H1CDR (26) GFN1KDSYMH (35)

H2CDR (50) WIDPENGDTEYAPKFQ (65)

H3CDR (99) GTPTGPYYFDY (109)

L1CDR (159) SASSSVSYMH (168)

L2CDR (184) STSNLAS (190)

L3CDR (223)QQRSSYPLT(231)

Fig. 1. Amino acid sequences of CAB1 CDRs

_		TUDOCHCURT	SCTASGENTK	DSYMHWLROG	PEQGLEWIGW
1	OAKTÖÖRRE	TAKSGISAKD	SCIASSINAN		TAVYYCNEGT
51	IDPENGDTEY	APKFQGKATF	TTDTSSNTAY		
101	PACEVAEUAM	GOGTTVTVSS	GGGGSGGGS		QSPAIMSASP
	CDIGUETECEN	CCCVCVMHMF	OOKPGTSPKL	WIYSTSNLAS	GVPARFSGSG
151		222421MIME	WOOD COVET	MECA COKT ET	KDAATDUSEK
201	SGTSYSLTIS	RMEAEDAATY	ACOOKSZILT	TEGMGIVDED	KRAATPVSEK
251	OLARWVANTT	TPIMKAOSVP	GMAVAVIYQG	KPHYYTFGKA	DIAANKPVTP
		remember CCD	ATARCETCI.D	DAVTRYWPOT.	TGKQWQGIRM
301	QTLFELGSIS	KTFTGVLGGD	ATARGETSED	DAVININGE	MDT VIVE OF C
351	T.DT.ATYTAGG	LPLOVPDEVT	DNASLLRFYQ	MMÖBÖMKBGI	TRLYANASIG
-		GMPYEQAMTT		TWINVPKAEE	AHYAWGYRDG
401			THE PART OF THE PA	MAN DENILLY DA	SLKQGIALAQ
451	KAVRVSPGML	DAQAYGVKTN			
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
DOI			AFIPEKQIGI		PARVEAAYHI
5.51	PVKASWVHKT	GSTGGFGSYV	WETLEVÖIGT	ALITERATOR	
601	LEALQ	•			

Fig. 2A Amino acid sequence of CAB1 protein

1	TPVSEKOLAE	VVANTITPLM	KAQSVPGMAV	AVIYQGKPHY	YTFGKADIAA
51	NKPVTPOTLE	ELGSISKTFT	GVLGGDAIAR	GEISLDDAVT	RYWPQLTGKQ
101	WOGTRMT.DT.A	TYTAGGLPLO	VPDEVTDNAS.	LLRFYQNWQP	QWKPGTTRLY
151	ANASTGLEGA	I.AVKPSGMPY	EQAMTTRVLK	PLKLDHTWIN	VPKAEEAHYA
201:	WGYRDGKAVR	VSPGMLDAOA	YGVKTNVQDM	ANWVMANMAP	ENVADASLKQ
251	GTAT.AOSRYW	RTGSMYOGLG	WEMLNWPVEA	NTVVETSFGN	VALAPLPVAE
301	VNPPAPPVKA	SWVHKTGSTG	GFGSYVAFIP	EKQIGIVMLA	NTSYPNPARV
351	EAAYHILEAL	Q			

Fig. 2B Amino acid sequence of BLA protein

H1CDR (26) GFNIKDSYMH (35)

H2CDR (50) WIDPENGDTEYAPKFQ (65)

H3CDR (99) GLPTGPYYFDY (109)

L1CDR (159) SASSSVSYMH (168)

L2CDR (184) DTSNLAS (190)

L3CDR (223) QQRDSYPLT (231)

Fig. 3A Amino acid sequences of CAB1.6 CDRs

H1CDR	(26) GFNIKDSYMH (35)
H2CDR	(50) WIDPENGDTEYAPKFQ (65)
H3CDR	(99) GLPLGAIYNDY (109)
L1CDR	(159) SASSAVYAMH (168)
L2CDR	(184) DTSNLAS (190)
L3CDR	(223) QQRDSYPLT (231)

Fig. 3B Amino acid sequences of CAB1.7 CDRs

1	OVOLOGSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
- 1	Z A Z D Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	APKFQGKATF	TTDTSSNTAY	LOLSSLTSED	TAVYYCNEGL .
51	-	GOGTTVTVSS		GGGGSENVLT	QSPAIVSASP
101	PTGPYYFDYW				GVPARFSGSG
151	GEKVTITCSA	SSSVSYMHWF			•
201	SGTSYSLTIS	RMEAEDAATY	YCQQRDSYPL	TEGAGTKLEL	KRAATPVSEK
251	OLAEVVANTI	TPLMKAQSVP	GMAVAVIYQG	KPHYYTFGKA	DIAANKPVTP
301	OTTERLESIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
•		LPLQVPDEVT		NWQPQWKPGT	TRLYANASIG
351					AHYAWGYRDG
401		GMPYEQAMTT		NMAPENVADA	SLKQGIALAQ
451		DAQAYGVKTN			PVAEVNPPAP
501		QGLGWEMLNW		SFGNVALAPL	
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ			• •	•

Fig. 4A Amino acid sequence of CAB1.6 protein

SEQ ID NO. 7

-					•
1	OVOLOOSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDTEY	APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGL
101		GQGTTVTVSS	GGGGSGGGS	GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF		VIYDTSNLAS	
201	SGTSYSLTIS	RMEAEDAATY	YCQQRDSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMAAQSVP		KPHYYTFGKA	
301	OTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT		NWQPQWKPGT	
401	LFGALAVKPS	GMPYEQAMTT	•	TWINVPKAEE	•
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET		•
551	PVKASWVHKT	GSTGGFGAYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALO		•	• ",	

Fig. 4B Amino acid sequence of CAB1.6i protein

			•		
1	OVOLOGSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	
51		APKFQGKATF	TTDTSSNTAY:	LQLSSLTSED	TAVYYCNEGL
101	PLGAIYNDYW	GQGTTVTVSS			QSPAIVSASP
151	GEKVTITCSA			VIYDTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRDSYPL		•
251	OLAEVVANTI	TPLMKAQSVP		KPHYYTFGKA	
301	OTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ		
401	LFGALAVKPS	GMPYEQAMTT		TWINVPKAEE	
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA		•
501	SRYWRIGSMY		PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	T.E.AT.O		- · · · · · ·	• .	

Fig. 5A Amino acid sequence of CAB1.7 protein

EWIGW CNEGL
CNEGL
VSASP
FSGSG
PVSEK
KPVTP
QGIRM
NASIG
GYRDG
IALAQ
NPPAP
IHYAA

Fig. 5B Amino acid sequence of CAB1.7i protein

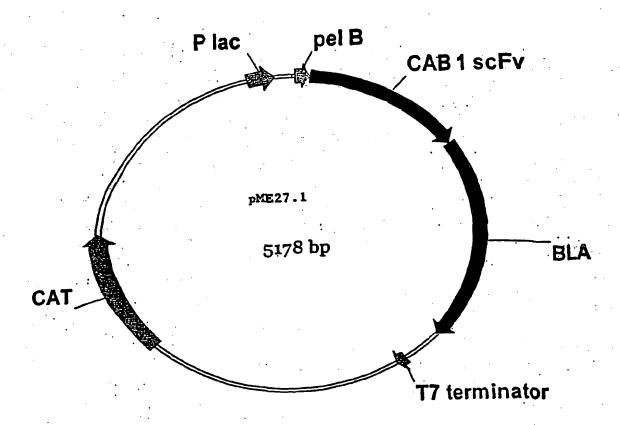


Figure 6A

	•		H	•		H2	•	8
Translation of CAB1	3	(1) QVRLQQSGARIVRSOTSVILSCIASOFSIKOSTHEMIRQQPBQGLSMIGHIDPENGDISYAPKEQGKATFITD786HTAY	SCINBORNIDBYA	STATE ROOFER	GIRMIGHIDE	DAGDTEY	APKEGGRAFFTTD RP T R	DTBBRTAY K
human consensus	3	9 2	S	9 4 >				:.
	•			•	•			
		81		:	linker	•	.•	일
Translation of CAB1	(81	(81) Lalsbetsedtavycabotptopxyddynggottvfvssgo	УТРТОРУТИРОТИВО	TTVTVBSOC		20SENVL	osgagosgagosbyvltospainbaspobkvtitcsa	BRVTITCBA
human consensus	(81)	AR				8	> 0	t
		161 L1	7				13	5
Translation of CAB1	(161	(161) SSEVETHINFQQKRGTSPKLMIYSTSHIASGVPARPSGSGGFSYSLFISRHSABDAATYYCQQRSSYPLIFGAGTKLSLAGAA	ILM TYSTSHIASON	parps6868	gtsyslfi srm	BABDAAT	YYCQQRBSYPLI	FOASTKLELTO
human consensus (161)	(161	A	•	A	4		_	.

Figure 6B

aggaattatcatatgaaat acctgctgccgaccgctgctgctgctgctgctcctcgctgcccagccggccatggcccaggtgaaactgcagcagt ctggggcagaacttgtga >cagggacctcagtcaagttgtcctgcacagcttctggcttcaacattaaagactcctatatgcactggtt gaggcagg ggcctgaacagggcctg gagtggattggatggattgatcctgagaatggtgatactgaatatgccccgaagttccagggcaaggccacttttactaca gacacatectecaacaca gectacetgeageteageageetgacatetgaggacaetgeegtetattattgtaatgagggacteegactgggeegt actactttgactactggggCcaagggaccacggtcaccgtctcctcaggtggaggcggttcaggcggaggtggctctggcggtggcggatcagaa aatgigctcacccagictc Cagcaatcatgictgcatctccaggggagaaggicaccataacctgcagtgccagctcaagtgtaagttacatgcactg gttccagcagaagccaggcacttctcccaaactctggatttatagcacatccaacctggcttctggagtccctgctcgcttcagtggcagtggatctgg gacctettacteteteacaateageegaatggaggetgaagatgetgecacttattactgecageaaagatetagttacecacteacgtteggtgetgg caccaagctggagctgaaacgggcggccacaccggtgtcagaaaaacagctggcggaggtggtcgcgaatacgattaccccgctgatgaaagc ccagictgttccaggcatggcggtatttatcagggaaaaccgcactattacacatttggcaaggccgatatcgcggcgaataaacccgtta cgcctcagaccctgttcgagctgggttctataagtaaaaccttcaccggcgttttaggtggggatgccattgctcgcggtgaaatttcgctggacgatg cggtgaccagatactggccacgtgacgggcaagcagtggcagggtattcgtatgctggatctcgccacctacaccgctggcggcctgccgcta caggtaccggatgaggtcacggataacgcctccctgctgcgcttttatcaaaactggcagccgcagtggaagcctggcacaacgcgtctttacgcca acgccagcatcggtcttttt ggtgcgctggcggtcaaaccttctggcatgccctatgagcaggccatgacgacgcggggtccttaagccgctcaagct ggaccatacctggattaacgtgccgaaagcggaagaggcgcattacgcctggggctatcgtgacggtaaagcggtgcgcgtttcgccgggtatgct ggatgcacaagcctatggcgtgaaaaccaacgtgcaggatatggcgaactgggtcatggcaaacatggcgccggagaacgttgctgatgcctcac ttaagcagggcatcgcgctgcgcagtcgcgctactggcgtatcgggtcaatgtatcagggtctgggctgggagatgctcaactggcccgtggagg ccaacacggiggicgagacgagitttggtaatgtagcactggcgccgttgcccgtggcagaagtgaatccaccggctcccccggtcaaagcgtcct gggiccataaaacgggctctactggcgggtttggcagctacgtggcctttattcctgaaaagcagatcggtattgtgatgctcgcgaatacaagctatc cgaacceggcacgcgttgaggcggcataccatatcctcgaggcgctacagtaggaattcgagctccgtcgacaagcttgcggccgcactcgagat casacgggctagccagccagaactcgcccgggaagacccgaggatgtcgagcaccaccaccaccaccactgagatccggctgctaacaaagc ccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttgggggcctctaaacgggtcttgaggggttttttgctgaaag gaggaactatatccggattggcgaatgggacgcgccctgtagcggcgcattaagcgcgggggggtgtggtggtggttacgcgcagcgtgaccgctacac ggttccgattlagtgctttacggcacctcgaccccaaaaaacttgattagggtgatggttcacgtagtgggccatcgcctgatagacggtttttcgccc tttgacgttggagtccacgttctttaatagtggactcttgttccaaactggaacaacactcaaccctatctcggtctattctttgatttataagggattttgcc gatticggcctatiggttaaaaaatgagctgatttaacaaaaatttaacgcgaattttaacaaaatattaacgcttacaatticctgatgcggtattttctcctt cgctgacgcgccttgacgggcttgtctgctcccggcatccgcttacagacaagctgtgaccgtctccgggagctgcatgtgtcagaggttttcaccgt catcaccgaaacgcgcgagacgaaagggcctcgtgatacgcctatttttataggttaatgtcatgataataatggtttcttagacgtcaggtggcactttt cggggaaatgtgcgcggaacccctatttgtttattttctaaatacattcaaatatgtatccgctcatgagacaataacccggggcagcatcacccgacg cacttigegeegaataaatacetgtgaeggaagateacttegeagaataaataaateetggtgteeetgttgataeegggaageeetgggeeaactttt ggcgaaaatgagacgttgatcggcacgtaagaggttccaactttcaccataatgaaataagatcactaccgggcgtatttttgagttatcgagattttca ggagctaaggaagctaaaatggagaaaaaaatcactggatataccaccgttgatatatcccaatggcatcgtaaagaacattttgaggcatttcagtca gttgctcaatgtacctataaccagaccgttcagctggatattacggcctttttaaagaccgtaaagaaaaataagcacaagtttatccggcctttattcac attettgeeegeetgatgaatgeteateeggaatteegtatggeaatgaaagaeggtgagetggtgatatgggatagtgtteaceettgttaeacegtttt ccatgagcaaactgaaacgtttcatcgctctggagtgaataccacgacgatttccggcagtttctacacatatattcgcaagatgtggcgtgttacggt gaaaacctggcctatttccctaaagggtttattgagaatatgttttcgtctcagccaatccctgggtgagtttcaccagtttgatttaaacgtggccaatat

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linker:

light chain:

envliqspaimsaspgekvtitcsasssvsymhwfqqkpgtspklwiystsnlasgvparfsgsgsgtsysltistmeaedaatyycqqtssypltfgagtklelkraat

pvsekqlaevvantitplmkaqsvpgmavaviyqgkphyytfgkadiaankpvtpqtlfelgsisktftgvlggdaiargeislddavtrywpqlfgkqwqgirmldlatytagglplqvpdevtd nasllrfyqnwqpqwkpgttrlyanasiglfgalavkpsgmpyeqamttrvlkplkldhtwinvpkaeeahyawgyrdgkavrvspgmldaqaygvktnvqdmanwvmannapenva daslkqgialaqsrywrigsmyqglgwemlnwpveantvvetsfgnvalaplpvacvnppappvkaswvhktgstggfgsyvaffpekqigivmlantsypnparveaayhilealq

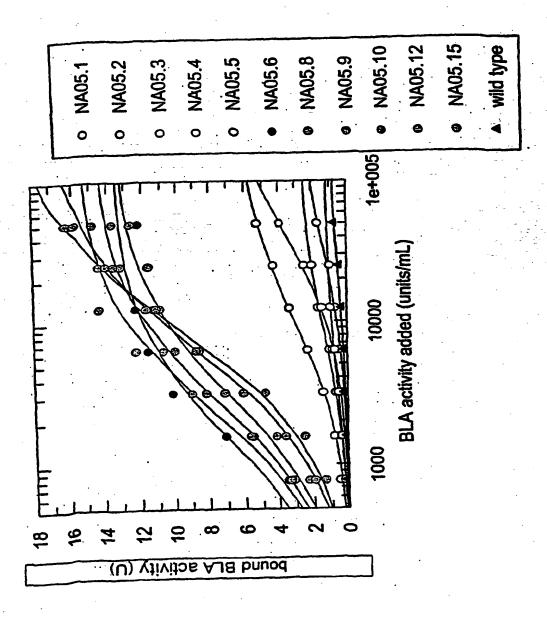
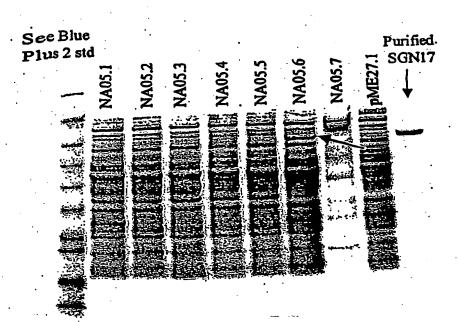


Figure7A

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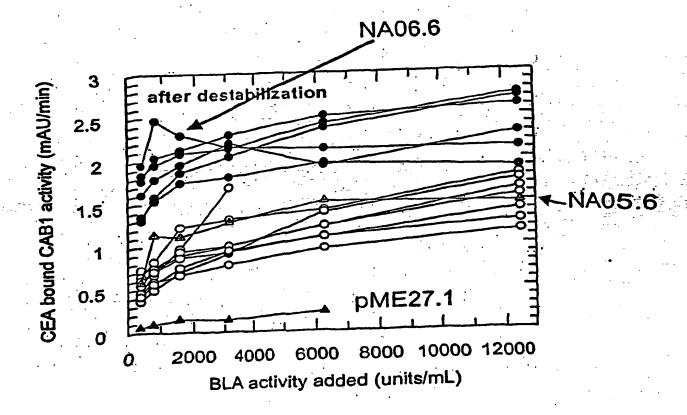


Figure 7C

		number of observations													1	1	
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1	81	힐								•		•		1	-		8
1	2	[2	-1	erved fre	onle	ncies of 5	mo	st abunde	and:	amio acid	is in :	alignmen	l of t	าบเกลก	CABI	COR	· <u>क</u>
	8	Ę	005	3, 100	,400.	,,0,00		seque	enes			•				<u> </u>	し旨
 			- 1	0.616	Q	0.346	D	0.014	G	0.014	A		L	0.003			
L	1	291	E	0.887	М	0.027		0.024	S	0.020		0.017	A	0.007			
_	2	293	V	0.852	H	0.034	Ā	0.027	T	0.027	E	. 0.014	V	0.014			F
<u> </u>	3	291	Q	0.975	V	0.011	Ä	0.007	D	0.004	M	0.004			:]		
L	4	282		0.645	a	0.148		0.120	A	0.022	M	0.014	N	0.014			
<u> </u>	5	276	Ž	0.693	0	0.263	Ā	0.022	D	0.011	G	0.007	R	0.004			
 	6	267	E	0.951	W	0.019	X	0.015	T	0.008	A	0.004	N	0.004			
<u> </u>	7	265	S	0.989	s	0.008	Ŧ	0.004							G.		
1	8	266	G	0.624	Ä	0.193	P	0.164	S	0.011	E	0.004	H	0.004			
-	9	274 271	9 G	0.638	E	0.192	D	0.081	Α	0.070	T	0.011	V	0.007			
-	-10	270	7	0.681	V	0.270	F	0.030	S	0.019]				L		
-	12	267	V	0.757	K	0.154	1	0.026	N	0.022	ايا	0.015	.A	0.007			L.
<u>}</u>	13	247	K	0.474	a	0.428	R	0.049	E	0.034	G	0.004	표	0.004		-	1
-	14	251	P	0.968	A	0.012	K	0.008	G	0.004	<u> </u>	0.004	S	0.004		<u> </u>	7
\vdash	15	244	G	0.783	S	0.156	T	0.033	P	0.016	K	0.008	Ē	0.004			╄
-	16	243	G	0.488	E	0.131	a	0.107	A	0.094	3	0.082	S	0.066			1
-	17	234	S	0.766	۲	0.204	Α	0.009	F	0.009	10	0.004	R	0.004	8	-	-
\vdash	18	244	L	0.812	V	0.155	M	0.008	A	0.004	m <	0.012	G	0.004	-	 	╄—
 	19	242	R	0.545	K	0.240	S	0.161	7	0.037	A	0.004	X	0.004		 	┼—
	20	246	L	0.736	>	0.191		0.061	Ш	0.009	Ä	0.005	Ö	0.005	s	 	
	21	218	S	0.729	-	0.234	S	0.009		0.000		- 0.000			C	1	+
	22	217	C	0.991	R	0.005	T	0.117	E	0.048	V	0.022	T	0.013	T	1	
L	23	231	A	0.558 0.638	Ŷ	0.174	G	0.064	寸	0.055	T	0.030	F	0.026			1
L	24	235	A	0.951	Ÿ	0.027	F	0.009	C	0.004	K	0.004	۲	0.004	S		
-	25	226	S	0.956	Ē	0.013	A	0.009	D	0.009	S	0.009	V	0.004			
-	26	225 213	F	0.559	Y	0.164	G	0.150	۵	0.080	S	0.019	<u> </u>	0.014			
-	27 28	203		0.571	S	0.286	1	0.049	2	0.049	P	0.015		0.005		-	
-	29	207	F	0.749	V	0.111	1	0.068	L	0.053	I	0.010		0.005		╀——	1
\vdash	30	202	S	0.762	T	0.119	N	0.035	G	0.020		0.020		0.010		 	1
1	31	199		0.482	T	0.136	О	0.104	N	0.087	G	0.060		0.040		HT	1
-	32	202	Y	0.535	S	0.144	N	0.083	<u>A</u>	0.069		0.031	무	0.030		H	
+	33		A	0.269	Y	0.162	G	0.147	8	0.117		0.091		0.040		Hi	╁╼┩
十	34			0:520	1	0.210	W	0.070	A	0.055						HI	╁┷┤
T	35			0.372		0.235		0.077		0.016		0.03				H2	├
ÌЗ	Ба	33	1:	0.824		0.096	V	0.043	_	0.032		0.005		0.00		H3	╂┷┤
	5b	27		0.856		0.064		0.037		, <u>0.032</u>	+~	+ -:	+ ••	1	W	1:5	
Γ	36			0.990		0.005	<u>. T</u>	0.005		0.005	10	0.005	,	 	L	+	1
Γ	37			0.741		0.228	L	0.005		1 - 5.550	╁╼	1-3.23	+-	1	Ā	1-	╆┵┦
. [38			0.989		0.005	<u>v</u>	0.005		0.005	: -	1	1-	+	là	1	╁┯┨
	39			0.979	T	0.011	<u>s</u>	0.003		0.052	_	0.010	ol v	0.01		+-	13
Γ	40			0.634		- 0.199		0.073		0.005		0.00				 	╆╣
Γ	41	187		0.914	_	0.043	<u>T</u>			0.005	_	+	1-	1	E	+-	17
	42			0.925	<u>s</u>	0.064	9	0.005		0.005	_	0.00	5		a	_	╆╣
Γ	43	186	K	0.683		0.183	R	0.124		0.027		1-5.55	+-	+	ੀਫ਼ੌ	+-	╆┥
Γ	44			0.882	<u>A</u>	0.048	S	0.043	1-	1 0.027	+-	+	Ť	1	L	+-	╆┥
	45	186		0.978		0.022	-	0.005	Ι	 	†	+	+		E	_	+
. Г	46	185		0.956		0.039	<u> </u>	0.005	 	 	+	+	+-	-	W	- 	+
	47	184	W	0.9891	S	0.011			<u>'</u>			<u> </u>	<u> </u>				

Figure 8A - \

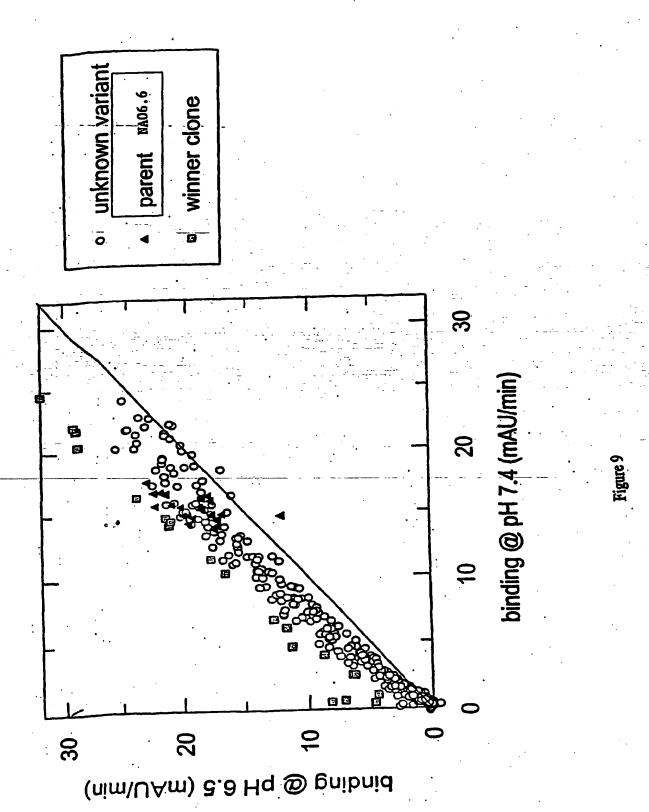
					_				0.124							
481	185	VI	0.481	_	0		0.173	느		-	0.005		0.005	-		
49	185	G	0.600		0.216		0.162	E	0.005	낡	0.003	Y	0.003		10	<u> </u>
50	185	R	0.146	W	0.146	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	0.119	A	0.114	밁				_	H2	
51	185	77	0.822	T	0.081	R	0.027	V	0.022	片		烘	0.011	_	H2.	
52	184	s	0.250	Y	0.239	N	0.123	<u> </u>	0.060	! 	0.054	뭐	0.050		H2	
	141	-	0.230		0.180	Y	0.153	G	0.126	N	0.066	<u> </u>	0.055	P	H2_	
52a	34	-1	0.814		0.115	R	0.060	G	0.005	Y	0.005				H2	
52b	22	-	0.880		0.044	V	0.033	S	0.022	A	0.011	G	0.005		H2	
52c		s	0.228		0.163	Y	0.125	G	0.109	N	0.082	H	0.054		H2_	
53	184	급	0.328		0.202	D	0.129	N	0.112	K.	0.082	F	0.055	_	H2	
54	183		0.544	S	0.181	D	0.085	W	0.066	Y	0.060	N	0.020	G	H2	
55	182	G	0.231	Ď	0.182	N	0.147	T	0.143	Y	0.077	G	0.060	D	H2	
56	182	S	0.582	K	0.120	N	0.065	À	0.054	1	0.054	P	0.022	T	H2	
57	184	<u></u>		N	0.216	D	0.139	R	0.060	H	0.055	T	0.038	E	H2	
58	183	Y	0.322	F	0.043	N	0.016	s	0.011	D	0.005	G	0.005		H2	7
59	184	Υ.	0.908		0.153	S	0.104	Ť	0.055	R	0.044	G	0.027	_	H2:	
60	183	A	0.579	NP	0.239	9	0.174	Ā	0.141	Ÿ	0.076	Ŧ	0.033	_	H2	
61	184	D	0.277		0.146	P	0.065	Ñ	0.038	G	0.016	R	0.016		H2	
62	185	S	0.686	_		F	0.215	S	0.011	Ā	0.005	K	0.005		H2	\vdash
63	186	<	0.511	능	0.247	R	0.054	N	0.032	E	0.022	T	0.022	_	H2	
64	186	K	0.581		0.237	T	0.032	Ä	0.016	D	0.011	E	0.011		H2	
65	186	G	0.688	S	0.054	H	0.005	~	0.005	_		•		K		1
66	186	R	0.935	10	0.409	1	0.065	Ė	0.054	A	0.005	8	0.005	A		1
67	186		0.462	L.Y.	0.038	A	0.016	S	0.011	ĸ	0.005	N	0.005			
- 68	186	I	0.914	1	0.139	v.	0.032	D	0.005	F	0.005	G	0.005			1
69	187		0.791	M	0.139	N	0.070	L	0.032	Ť				T		М
70		S	0.684	V	0.160	Ä	0.107	P	0.064	T	0.053	K	0:043	T	1	-:1
71	187	R	0.529	N	0.071	ĸ	0.016	E	0.011	-				D		-
. 72	186	D	0.368	N	0.266	Ď	0.177	K	0.070	E	0.059	A.	0.011	T		
73		T	0.946	A	0.04B	1	0.005						· ·	S		
74		S	0.674	÷	0.139	7	0.070	R	0.027	A.	0.021	F	0.021	S		1
75		K	0.701	s	0.251	K	0.027	R	0.011	T	0.005	Y	0.005	N		
76		N	0.615	G	0.273	s	0.048	M	. 0.021	L.	0.016	P	0.011	T		
77		1.	0.364	Ā	0.273	F	0.235	V	0.096		0.005	M	0.005	Α		
78	-		0.638	S	0.239	F	0.059	V	0.048	H	0.005	M	0.005	Y		
79		Y	0.782	м	0.207	N	0.005	•	0.005					L		
80		_	0.529	E	0.205	K	0.122	R	0.032	T	0,032	N.	0.027	Q.		
81	187	10	0.497	ᆫ	0.421	W	0.051	7	0.015	1	0.010		0.005	L	\	
82		_	0.442	S	0.291	R	0.077	-	0.066	D	0.053	G	0.020			
82a	195		0.795	N	0.082	R	0.051	G	0.026	T	0.021	A	0.010	S		
82b	194		0.701	♡	0.234	M	0.041	G	0.010	Α	0.005		0.005			
82c	197		0.528	Ť	0.239	K	0.122	D	0.041	E	0.020	Q	0.015			
83	1	1	0.328		0.182	_	0.177	T	0.051	1	0.035		0.030			
. 84			0.591	<u> </u>	0.172		0.126		0.051		0.045	G	0.015	E		\Box
85			0.975		0.010	V	0.010		0.005		1			D		
86			0.929		0.035		0.010		0.010		0.005	Q	0.005	T	1	
87					0.040		0.005		0.005		0.005				1	
88			0.939		0.066		0.056	_	0.045		0.040		0.010			
89			0.768				0.005		0.005		 	1	7	Y	1	┼─┤
90			0.980		0.010				0.005		0.005	:1-	1	Ý	1	╅
91	199	Y	0.930		0.045		0.015		0.005	├	0.000	1	 	tc	1	╅
92			0.990		0.005		0.005		0.000	1	0.005	N	0.005		 	╁╌╢
93			0.838	T	0.076	V	0.061	_	0.005							11
94			0.596	K	0.162	T	0.051		0.045		0.045				 	11
95			0.174	D	0.120	E	0.099		0.093		0.092				1	\vdash
96			0.168		0.130	G	0.112		0.062		0.062				IH3	∐
97				P	0.094	V	0.094	E	0.088		0.069				нз	\sqcup
				YI	0.101	L	0.095	D	0.087	V	0.076	<u> </u>	0.063	II	НЗ	
98	135	1 6	!	<u> </u>	······································									•		

observed frequencies of 5 most abundand amio acids in a sequenes 1 95 Q O.589 S 0.158 N 0.095 H 0.074 D 2 139 S O.446 Y 0.388 F 0.101 V 0.043 L 3 140 V O.307 E 0.243 A 0.207 M 0.093 D 4 140 L O.971 V 0.029 5 141 T O.915 A 0.021 S 0.021 I 0.014 K 6 140 Q O.993 E 0.000 S 0.029 A 0.022 F	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N 0.043 V	CAB1 sequence	mutated residues
observed frequencies of 5 most abundand amio acids in a sequenes 1 95 Q O.589 S 0.158 N 0.095 H 0.074 D 2 139 S O.446 Y 0.388 F 0.101 V 0.043 L 3 140 V O.307 E 0.243 A 0.207 M 0.093 D 4 140 L O.971 V 0.029 5 141 T O.915 A 0.021 S 0.021 I 0.014 K 6 140 Q O.993 E 0.007	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	CAB1 sequence	mutated residues
observed frequencies of 5 most abundand amio acids in a sequenes 1 95 Q O.589 S 0.158 N 0.095 H 0.074 D 2 139 S O.446 Y 0.388 F 0.101 V 0.043 L 3 140 V O.307 E 0.243 A 0.207 M 0.093 D 4 140 L O.971 V 0.029 5 141 T O.915 A 0.021 S 0.021 I 0.014 K 6 140 Q O.993 E 0.007	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	CAB1 sequence	mutated residues
observed frequencies of 5 most abundand amio acids in a sequenes 1 95 Q O.589 S 0.156 N 0.095 H 0.074 D 2 139 S O.446 Y 0.388 F 0.101 V 0.043 L 3 140 V O.307 E 0.243 A 0.207 M 0.093 D 4 140 L O.971 V 0.029 5 141 T O.915 A 0.021 S 0.021 I 0.014 K 6 140 Q 0.993 E 0.007	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	CAB1 sequen	mutated resid
observed frequencies of 5 most abundand amio acids in a sequenes 1 95 Q O.589 S 0.156 N 0.095 H 0.074 D 2 139 S O.446 Y 0.388 F 0.101 V 0.043 L 3 140 V O.307 E 0.243 A 0.207 M 0.093 D 4 140 L O.971 V 0.029 5 141 T O.915 A 0.021 S 0.021 I 0.014 K 6 140 Q 0.993 E 0.007	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	CAB1 sequ	mutated re
1 95 Q O.589 S U.158 N U.505 N	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	CAB! S	mutated
1 95 Q O.589 S U.158 N U.505 N	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	880	muta C
1 95 Q O.589 S U.158 N U.505 N	0.053 F 0.014 T- 0.064 I	0.021 E 0.007 N	3 5	5 E
1 95 Q O.589 S U.158 N U.505 N	0.014 T- 0.064 I	0.007 N		1
2 139 S O.446 Y 0.388 F 0.101 V 0.043 L 3 140 V O.307 E 0.243 A 0.207 M 0.093 D 4 140 L 0.971 V 0.029 5 141 T 0.915 A 0.021 S 0.021 I 0.014 K 6 140 Q 0.993 E 0.007	0.064	0.007 N 0.043 V	· - -	
3 140 V 0.307 E 0.243 A 0.207 M 0.093 D 4 140 L 0.971 V 0.029 5 141 T 0.915 A 0.021 S 0.021 I 0.014 K 6 140 Q 0.993 E 0.007		0.043		1
4 140 L 0.971 V 0.029 5 141 T 0.915 A 0.021 S 0.021 I 0.014 K 6 140 Q 0.993 E 0.007	0.007 L	•=		
5 141 T 0.915 A 0.021 S 0.021 I 0.014 K	1 0.0071 L	0 000		
6 140 Q 0.993 E 0.007		0.007 T		
	0.014	S		
7 139 P 0.906 D 0.029 S 0.029 A 0.022	0.014 0.007 S	0.007 P		
B 139 P 0.741 A 0.137 H 0.072 H 0.029 C	10.00/	0.007 P		+
9 139 S 0.964 A 0.014 V 0.014 H 0.007	+	1 1 P		
10 0 - 1.000 0 0.000 M 0.014	 	M		+
11 138 V 0.790 A 0.136 E 0.007 E 0.004 Q	0.004	S	-:- -	1
12 139 S 0.370 C 0.348 A 0.138 F 0.087 L	0.014 D	0.007 A	_	-
13 138 V 0.007 A 0.230 T 0.111 D 0.007 F	0.007 G	0.007 S	11.1	
14 135 8 0.000 4 0.000 5 0.007		P		
15 135 P 0.007	1 - 1	G		
16 134 G 0.811 K 0.098 A 0.045 E 0.024 G	0.015 H	0.008 E		7
17 133 C	0.008 G	0.008 K		1
18 130 V 0.454 A 0.385 1 0.146 G 0.008 L	0.008	V 216		
20 128 T 0.531 R 0.188 S 0.148 K 0.047 I	0.031 M	0.016 T		
21 121 0.901 V 0.050 L 0.017 A 0.000 I	0.008 M 0.008 N	0.008 T	- -	
22 120 S 0.492 1 0.475 A 0.008 G 0.500 I	0.006	0.005 T		
23 117 C 1.000 T 0.050 G 0.080 A 0.045 Q	0.033	0.018 8	Li	
.24 112 S 0.370 I 0.056 B 0.028 A 0.019 I	0.009 P	0.009 A	Li	
25 108 G 0.000 S 0.250 T 0.213 N 0.087 E		0.037 \$	Li	
26 108 D 0.555 N 0.118 K 0.113 A 0.104 T	0.066 G	0.047 8	Li	
27 104 S 0.346 S 0.346 J 0.115 G 0.067 A		0.019 S	Li	
28 104 C 0.243 N 0.239 D 0.159 S 0.078 P		0.058 V		
28 100 G 0.291 V 0.165 D 0.136 N 0.107 E		0.049 8		
30 103 1 0.356 K 0.168 A 0.099 E 0.084 Q		0.069 Y		
319 54 0.438 S 0.167 G 0.104 N 0.083 Y		0.052 M		
0.495 N 0.227 Y 0.155 S 0.041 G		0.021 H		
31c 23 - 0.760 N 0.134 S 0.031 K 0.021 D	U.U.Z. E	0.010	11	
31d 0 - 1.000		++	L1	
31e 0 - 1.000		 -	L1	
311 0 - 1.000 T	0.052 H	0.041	L1	
32 94 Y 0.515 S 0.134 P 0.093 A 0.072		0.010	L1	
33 97 V 0.680 A 0.186 1 0.082 1 0.021 1		0.076	L1	
34 92 S 0.380 H 0.120 A 0.109 1 0.096 14		U.O.O		┽┦
35 98 W 0.990 Y 0.010		F		+
36 96 Y 0.844 F 0.073 H 0.073 W 0.010	0.011 Y	0.011 C		+
37 95 Q 0.916 R 0.042 E 0.011 H 0.011 K		0.011		+
38 94 Q 0.862 H 0.053 L 0.053 E 0.011 K		0.043 K		+
30 93 K 0.333 L 0.172 H 0.101 H 0.131		P		+
40 93 P 0.946 S 0.022 A 0.011 L 0.011 R				

												_			-		
						D	0.022	RI	0.022	P	On-) [0.011	G		T	
41	93	G	0.871	<u>H</u>	0.012	K	0.163	R	0.087	S	0.0	G	0.022	T		T-	٦
42	92	a	0.424	I	0.217		0.065	Ť	0.022	Ī	0.011	V	0.011	S	·		コ
43	92	A	0.717	S	0.174	G	0.003	 -						P			٦
44	93	P	0.978	Α	0.011	M	0.109		0.065	T	0.065	A	0.033	K		_	٦
45	92	K	0.391	V	0.315	R		누	0.043	À	0.022	M	0.022			 	٦
46	92	L	0.728	٧	0.076	<u>. F</u>	0.065			N	0.011			W	 	 -	귀
47	91	V	0.484	L	0.374		0.077	M	0.055		0.011			F	 -	╀┯╌	긤
48	91	-1	0.791	>	0.110	M	0.077	<u> </u>	0.011	S	0.011	-, - 	0.011	.	!	 	┪
49	91	Ÿ	0.769	F	0.110	R.	0.066	<u> H</u>	0.022	밁	0.056	ĸ	0.056	-	12	 	4
50	89	Ď	0.303	E	0.210	Q	0.093		0.067	G		G				 	-1
	88	D	0.364	N	0.205	~	0.159	H	0.068	Ţ	0.068		0.034		12	<u></u>	4
51	89	N	0.393	. T	0.213	S	0.202	D	0.101	A	0.022	<u>F</u>	0.011	_	12		4
52		K	0.307	0	0.193	a	0.182	N	0.080	E	0.057	S	0.057	N_	12		4
53	88	R	0.875	X	0.068	K	0.034	L	0.011	W	0.011			<u> </u>	12		4
54		P	0.851	G	0.080	S	0.023	A	0.011	Н	0.011	R	0.011		12	<u> </u>	4
55	86		0.837	B	0.081	P	0.023	A	0.012	<u> </u>	0.012	T	0.012		12		┙
56	85	0	0.920	Ē	0.034	S	0.011	T	0.011	W.	0.011		0.011			<u></u>	4
57	86	G	0.600		0,353	Ä	. 0.012	G	0.012	T	0.012	•	0.012		.		┛
58		P	0.847	S	. 0.106	A	0.012	L	0.012	٧	0.012	•	0.012			<u> </u>	L
59			0.488	E	0.325	·N	0.047	Α	0.035	H	0.023	<u> </u>	0.023		 	1	Ц
60		R	0.977	B	0.011	-	0.011					•		R	<u> </u>		4
61		F	0.943	1	0.034	L	0.011	R	0.011					F.		<u> </u>	4
62		S	0.989	F	0.011	· · ·								8	<u> </u>	<u> </u>	1
63		G	0.885	A	0.069	S	0.023	·V	0.023			·		G			4
64		S	0.977	G	0.011	Y	0.011				I			S			4
65			0.430	N	0.186	S	0.186	. T	0.081	X	0.070	R	0.035	G.		7	4
67			0.953	T	0.024	K	0.012	L	0.012		0.000	-		S			4
6	_		0.859	S	0.071	A	0.035	D	0.024	Q	0.012		0.004	G			4
65			0.434	T	0.318	.A	0.129	_D_	0.036	G	0.024	K	0.024	S	 _ _		4
70			0.529	S	0.341	E	0.082	<u>A</u>	0.024	K	0.024		 	Y			Н
7			0.847	T T	0.082	<u>_v</u>	0.059	S	0.012	 -	0.012		 	S		<u>-</u>	4
7			0.447	S	0.424	Y	0.082	Α.	0.035	 -	0.012			L			4
75			0.988	S	0.012	<u> </u>	 		0.012		0.012			Ħ			1
74			0.706	Α	0.165	G	0.106		0.012		0.012		 	 	 		1
75			0.929	٧	0.047	A	0.012	<u> </u>	0.012	G	0.012	R	0.012	s			ł
70			0.718	-1	0.200	<u>N</u>	0.035	-1-	0.024		0.0.2		0.0.2	Ř	\vdash		1
7			0.765	R	0.129	<u>s</u>	0.094	E_	0.071	G	0.012	 	 	M		.1	ſ
7			0.588	.٧	0.224	<u></u>	0.106	K·	0.071	 ~	0.024	A	0.012		 		1
79			0.659	ш	0.153	R	0.071	<u>V</u>	0.047	声	0.035		0.012				1
80			0.459	S	0.235		0.200	-	0.047		0.024		0.024		 - 	 -	1
8			0.541	G	0.235	<u>M</u>	0.071		1 0.047	┼	1	' 	1	D			1
8			0.964	<u> </u>	0.024	<u> E.</u>	0.012			 	1 ===	1		Ā		- 1	1
8		_	0.976		0.012	<u> </u>	0.012	s	0.012	+	1	1	T .	A	 		١
8			0.941		0.035	E	0.012		0.012		0.012	M	0.012			1	1
8			0.859	E	0.082	_ H_	0.024	Α_	0.012	+	1	T	1	Y	┝╌┼		1
8			0.976	F	0.012	H	0.012		 	+	 	 	1	Ÿ	 		1
8			0.894	F	0.106		 		 	+	+		 	Ċ			l
B			0.988	H	0.012				0.004	+-	0.059	N	0.035		L3		ı
 8			0.482	A	0.153		0.141	G	0.094				0.035				l
1-8			0.388		0.271	Α	0.212	V	0.118		0.012		0.000	0	L3		
- 5			0.576		0.247	Α	0.059	F	0.035		0.035		0.012		13		ĺ
			0.606		0.095	Α	0.071	N	0.061		0.048		0.024		L3		
9					0.179	G	0.107	N	0.095		0.071		0.060		13		
9			0.536		0.155	N	0.073	R	0.060		0.058		0.048		L3		Į
9					0.253	G	0.108	N	0.096	T	0.084	<u>I A</u>	0.036	IP.	L3		
<u>_ 9</u>	5 8	2 S	1 0.200											•	· _ 		

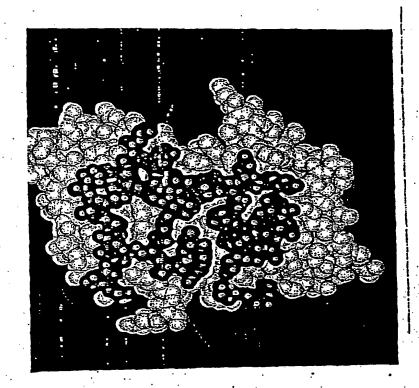
Figure 8B - 2

•			•	-									2 242		7	
· .— ·			0601	SI	0.183	-D 1	0.159	N	0.110	T	0.073	<u>a</u>	0.049		L3	
95a	60	- 1	0.268		0.098	G	0.098	H	0.085	E	0.049	R	-0.037		L3	
95b	40	-	0.512	<u>A</u>	0.037	Ā	0.012	G	0.012						L3	
95c	5	- 1	0.939	<u> </u>			- 0.0								L3	
95d	1	- 1	0.988	G	0.012										L3	
95e	Ö		1.000		<u>·</u>				 						L3	
951	- 6		1.000				0.000	W	0.098	A	0.073	N	0.073		L3	
96	80	V	0.305	G	0.098	<u> </u>	-0.098	M	0.035	G	0.012	•			L3	_
97	85	Ÿ	0.788	1	0.118	L	0.047		0.055		1		1	F	+==+	
	86	F	0.988	· V_	0.012	·					1			G	╀╌┦	
98		Ġ	0.989	F	0.011				0.022				1	A	+	
99	89	_ G _	0.831	·T	0.124	Α	0.022	S	U.UZZ					G	+	 '
100	89		1.000			- '					 		+	7	╂┷┥	
101			0.989	G	0.011				0.004		0.034	E	0.011	k	╅━┤	
102			0.739	N	0.091	R	0.068	Q	0.034	<u> '-</u> -	0.034	-	1 0.011	li`	╂┯┥	
103		-	0.667	V	0.322	Q	0.011					-	 	E	+	
104		 	0.954	S	0.023	1	0.011	<u> </u>	0.011		-		 	 	╂	
105			0.988	T	0.012							ļ	 	K	+	
106			0.952	V	0.024	Ρ	0.012	Q	0.012		0010		+	A	┽┷┥	
1068	84		0.782	S	0.103	R	0.090	Ö	0.013	1	0.013	}		A	╃┷┤	
107			0.957	P	0.022	R	0.022			ļ:		-	 	Â	+	
108			0.957	K	0.022	a	0.022		 	↓	4	+	 	+	+	
109	46	P	1-0.007						<u> </u>	1	<u> </u>	-	+	┿	╅┯┥	
		 -	1						<u> </u>	<u> </u>		نبت			1	
	1			·					•• • •		· -:'	•			•	



CDRs in NA06.6

Residues chosen for mutagenesis in NA06.6



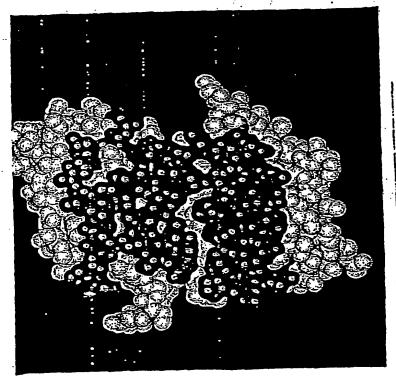
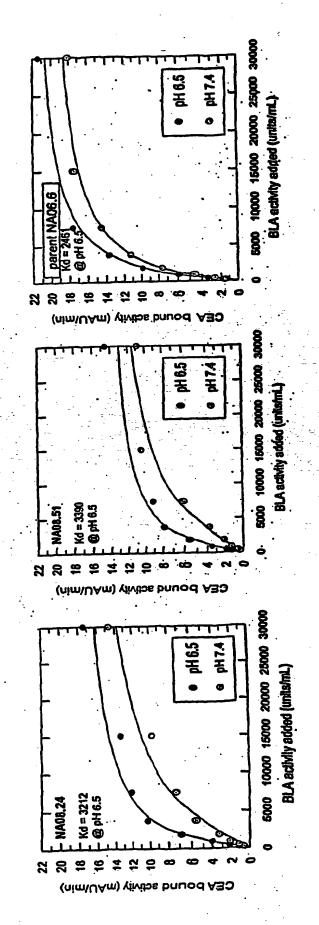


Figure 10

BLA activity added (units/mL)

BLA activity added (units/mL)

BLA activity added (units/mL)



PH 7.4 pH.6,5

2 2 2 2 2

PH 6.5 PH 7.4

Kd = 9978 @ pH 8.5

Kd = 4690 Q pH 6.5

(CEA bound activity (mAU/min)

CEA bound activity (mAU/min)

pH 6.5 PH 7.4

CEA bound activity (mAUlmin)

cumulative changes

Figure 12: CAB1 engineering - summary

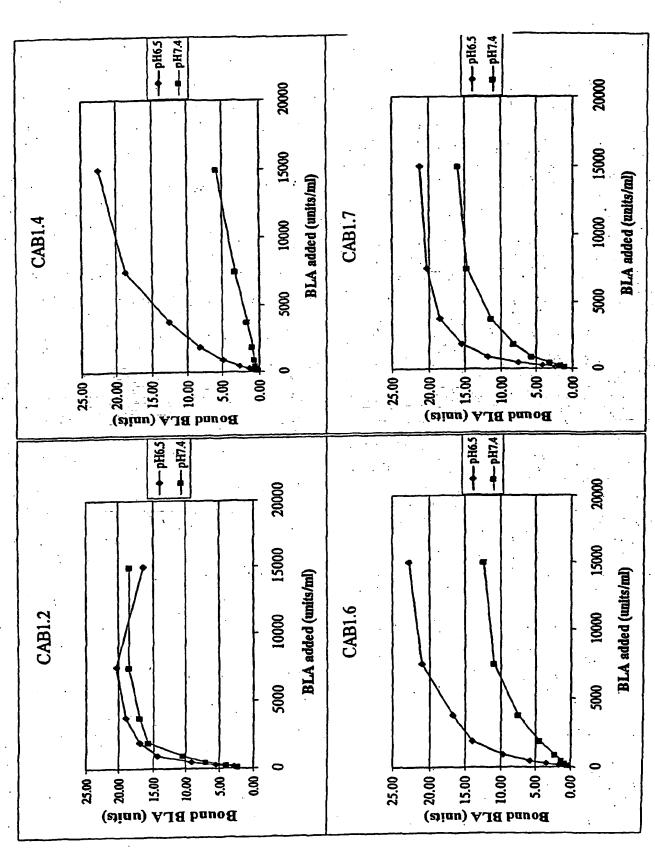
protein	changes	comments
CAB1	parent	
CAB1.1(NA05.6)	CAB1.1(NA05.6) R13K, T16G, W181V	increase stability
CAB1.2(NA06.6)	CAB1.2(NADG.6) K3Q, L37V, M146V	increase stability
CAB1.4(NA08.15)	CAB1.4(NA08.15) S184D, S226D	pH-dependent binding
CAB1.6	T100L	increased affinity
SW149.5	T102L, P104A, Y105I, F107N	increased affinity
CAB1.7	S163T, S165Y, Y166S	increased affinity
CAB1.7i	in BLA: K265A, S568A	remove T-cell epitopes

BLA activity (units/mL)

BLA activity (units/mL

Figure 13: Binding of various CAB1 variants to immobilized (2000 4000 6000 8000 10000 12000 14000 PH 7.4 Kd ≈ 3008 pH 6.5 Kd = 1197 pH 7.4 Kd = 61789 pH 6.5 Kd = 9298 BLA activity (units/mL **CAB1.4** 2225 CEA binding (units) CEA binding (units) 2000 4000 6000 8000 10000 12000 14000 pH 7.4 Kd = 119917 pH 6.5 Kd = 1323 pH 7.4 Kd = 2210 pH 6.5 Kd = 5518 BLA activity (units/mL) **CAB1.6** 4 2 2 2 2 4 CEA binding (units) CEA binding (units)

Figure 14: Binding of various CAB1 variants to LS174T cells



•	OVOT OOSGAE	TAKSGGSVKI	SCTASGENIK	DSYMHWVRQG	PEQGLEWIGW	
1	O ∧ OTO O O O O O O O O O O O O O O O O	PAKEOCRIME	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGL .	
51			11010001111	CCCCENTI	OSPAIVSASP	
101	PLGAIYNDYW	GQGTTVTVSS		GGGGSENVLT		
151	GEKVTITCSA	SSSVSYMHWF	QQKPGTSPKL	VIYDTSNLAS	GVPARFSGSG	
	CCMCVSIMIS	RMEAEDAATY	YCOORDSYPL	TFGAGTKLEL	KRAATPVSEK	
201			CHANNAUTYOC	KPHYYTFGKA		
251	QLAEVVANTI	TPLMKAQSVP				
301	OTT.FELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL		
			DNASLLRFYQ	NWQPQWKPGT	TRLYANASÍG	
351		LPLQVPDEVT				
401	T.FGALAVKPS	GMPYEQAMTT	RVLKPLKLDH		AHYAWGYRDG	
451		DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ	
			PVEANTVVET	SFGNVALAPL	PVAEVNPPAP	
501	SRYWRIGSMY	QGLGWEMLNW				
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI	
		•				
601	LEALQ			• •		

Fig. 15A Amino acid sequence of SW149.5 protein

			•	· ·	
· 1	OVKLOOSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWLRQG	PEQGLEWIGW
51		APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
	PTGPYYFDYW	GQGTTVTVSS	GGGGGGGG	GGGGSENVLT	OSPAIMSASP
101			OOKPGTSPKL	VIYSTSNLAS	GVPARFSGSG
151	GEKVTITCSA		QQRFGISFILL		
201.	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI		GMAVAVIYQG	KPHYYTFGKA	DIAANKPVTP
301		KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
			DNA ST.T.REYO	NWQPQWKPGT	TRLYANASIG
351		LPLQVPDEVT			
401	LFGALAVKPS.	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAEE	ARIAWGIRDG
451		DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
		QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
501	SKIWKIGSMI	CODOME PROPERTY		VMLANTSYPN	
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	AMMINITAL	T torris management
601	LEALQ				

Fig. 15B Amino acid sequence of CAB1.1 protein

	•					
1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC	
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA	
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG	
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA	
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA	
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT	
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC	
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG	
401	GATCAGAAAA.	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA	
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT	
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATA	
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA	
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC	
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG	
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAA	
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA	
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT	•
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT	
901	CAGACCCTGT	TCGAGCTGGG	TICINIMA	AAAACCTTCA	CCGGCGTTTT	
. 951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA	
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG	
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA AACTGGCAGC	
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	CAGCATCGGT	
1151	CGCAGTGGAA			ACGCCAACGC	· · · · · · · · · · · · · · · · · · ·	
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT GCTGGACCAT	ACCTGGATTA	
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	CCTGGGGCTA	TCGTGACGGT	
1301	ACGTGCCGAA		GCGCATTACG	GATGCACAAG	CCTATGGCGT	
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GGTCATGGCA	AACATGGCGC	
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG	
1451	CGGAGAACGT	TGCTGATGCC	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT	
1501	TCGCGCTACT	GGCGTATCGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA	
1551	GCTCAACTGG	CCCGTGGAGG	CCCATGGCAG	AAGTGAATCC	ACCGGCTCCC	
1601	ATGTAGCACT	GGCGCCGTTG	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG	
1651	CCGGTCAAAG	CGTCCTGGGT	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG	
1701	CAGCTACGTG	GCCTTTATTC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC	
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	110200000		
1801	CTCGAGGCGC	TACAG		•	• • •	

Fig. 15C Nucleotide sequence of CAB1.2 gene

1	OVOLOOSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51		APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101	PTGPYYFDYW	GOGTTVTVSS	GGGGSGGGS	GGGGSENVLT	
151	GEKVTITCSA	SSSVSYMHWF	QQKPGTSPKL	VIYSTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	OLAEVVANTI		GMAVAVIYQG.	KPHYYTFGKA	DIAANKPVTP
301	OTLFELGSIS			DAVTRYWPQL	
351	LDLATYTAGG			NWQPQWKPGT	
401	LFGALAVKPS			TWINVPKAEE	
451		DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	
501		QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	T.EALO		•	1 1 1 -	•

Fig. 15D Amino acid sequence of CAB1.2 protein

H1CDR (26) GFNIKDSYMH (35)

H2CDR (50) WIDPENGDTEYAPKFQ (65)

H3CDR (99) GTPTGPYYFDY (109)

L1CDR (159) SASSSVSYMH (168)

L2CDR (184) DTSNLAS (190)

L3CDR (223) QQRDSYPLT (231)

Fig. 15E Amino acid sequences of CAB1.4 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)

L1CDR (553)AGTGCCAGCTCAAGTGTAAGTTACATGCAC(582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15F Nucleotide sequence of CAB1.4 CDRs

	_		•		
1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GCCGTGGCG
401	GATCAGAAAA.	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATG
551	ATACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
. 951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA TATTCGTATG
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	AGGTACCGGA
1051	CTGGATCTCG	CCACCTACAC		CTGCCGCTAC CTTTTATCAA	AACTGGCAGC
1101	TGĄGGTCACG	GATAACGCCT	CCCTGCTGCG	ACGCCAACGC	CAGCATCGGT
1151	CGCAGTGGAA		ACGCGTCTTT	GGCATGCCCT	
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GCTGGACCAT	ACCTGGATTA
1251	CATGACGACG	CGGGTCCTTA		CCTGGGGCTA	TCGTGACGGT
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1351	AAAGCGGTGC	GCGTTTCGCC	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1401	GAAAACCAAC	GTGCAGGATA	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1451	CGGAGAACGT	TGCTGATGCC	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1501		GGCGTATCGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1551	GCTCAACTGG	CCCGTGGAGG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1601	ATGTAGCACT	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1651	CCGGTCAAAG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1701	CAGCTACGTG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1751	CGAATACAAG		COGGCACGCG		
1801	CTCGAGGCGC	TACAG,		,	. : .

Fig. 15G. Nucleotide sequence of CAB1.4 gene

1	OVOLOOSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDTEY	APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101		GQGTTVTVSS		GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA		QQKPGTSPKL		GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY			KRAATPVSEK
251	OLAEVVANTI	TPLMKAQSVP	GMAVAVIYQG		DIAANKPVTP
301		KTFTGVLGGD			TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT		NWQPQWKPGT	
401	LFGALAVKPS	GMPYEQAMTT		TWINVPKAEE	
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	
501	SRYWRIGSMY	QGLGWEMLNW		SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ		•	•	

Fig. 15H Amino acid sequence of CAB1.4 protein

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGCTCCCGACTGGGCCGTACTACTTTGACTAC (405)

L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG(771)

Fig. 15I Nucleotide sequences of CAB1.6 CDRs

1	CAGGTGCAGC	TGCAGCAGTC		CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA.	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATG
551	ATACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA.
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
. 951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC		AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA		ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT		ATGAGCAGGC
1251-	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG GCTGGGAGAT
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	AGTTTTGGTA
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG GTGATGCTCG
1701	CAGCTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Fig. 15J Nucleotide sequence of CAB1.6 gene

·				_
CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA		CAGGGGGCTC
	TCCTGCACAG	CTTCTGGCTT	•	GACTCCTATA
	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
		CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
		ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
		TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
=	- :	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
		CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
		CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
			TCCCAAACTC	GTGATTTATG
			CTCGCTTCAG	TGGCAGTGGA
		CACAATCAGC	CGAATGGAGG	CTGAAGATGC
		AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
		AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
		GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
		TGGCCGTTAT	TTATCAGGGA	AAACCGCACT.
		GATATCGCGG	CGAATAAACC	CGTTACGCCT
	TCGAGCTGGG	TTCTATAAGT		CCGGCGTTTT
	GCCATTGCTC	GCGGTGAAAT		GATGCGGTGA
	GCCACAGCTG	ACGGGCAAGC		TATTCGTATG
	CCACCTACAC	CGCTGGCGGC		AGGTACCGGA
	GATAACGCCT	CCCTGCTGCG		AACTGGCAGC
CGCAGTGGAA	GCCTGGCACA			CAGCATCGGT
CTTTTTGGTG	CGCTGGCGGT		- · · · · · · · · · · · · · · · · · · ·	ATGAGCAGGC
CATGACGACG				ACCTGGATTA
ACGTGCCGAA	· ·			TCGTGACGGT
AAAGCGGTGC				CCTATGGCGT
GAAAACCAAC	- -			AACATGGCGC
			•	GCTGGCGCAG
-	- - ·			GCTGGGAGAT
				AGTTTTGGTA
				ACCGGCTCCC
- .	-			GCGGGTTTGG
CGCGTACGTG		01 0.40		GTGATGCTCG
	•	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
CTCGAGGCGC	TACAG			
	GGGGAGAAGG GCACTGGTTC ATACATCCAA TCTGGGACCT TGCCACTTAT CTGGCACCAA CAGCTGGCGG GTCTGTTCCA ATTACACATT CAGACCCTGT AGGTGGGGAT CCAGATACTG CTGGATCTCG TGAGTCACG CGCAGTGGAA CTTTTTGGTG CATGACGACG ACGTGCCGAA AAAGCGGTGC GAAAACCAAC CGGAGAACGT TCGCGCTACT GCTCAACTGG ATGTAGCACT CCGGTCAAAG	AGTCAAGTTG TGCACTGGGT GAGGCAGGGG ATTGATCCTG AGAATGGTGA GGCCACTTTT ACTACAGACA GCAGCCTGAC CCGACTGGGC CGTACTACTT CCGACTGGGC CGTACTACTT GAGCAGAAAA TGTGCTCACC GGGGAGAAGG GCACTGGTC ATACATACC GCACTGGTC CAGCAGAAAGC CAGCAGAAAGC ATACATCCAA TCTGGGACCT TCTGGGACCT TTACTCTCT TGCCACTTAT TACTGCCAGC CAGCTGGCGG AGGTGGTGCG GTCTGTTCA CAGCAGAGCC CAGCTGGCGG AGGTGGTC CAGCAGAGCC CAGCTGGCGG AGGTGGTCGC CAGCTGGCGG ATTACACATT CCAGATACTC CAGATACTC CAGATACTC CAGATACTC CCAGATACTC CCAGATACTC CCAGATACTC CCAGATACTC CCAGATACTC CCAGATACTC CCACCTACAC CTTTTTGGTG CCACCTACAC CTTTTTTGGTG CGCTGGCGT ACGTGCCGAA AGCGGAAGAC CTTTTTTGGTG CGCTGGCGT CCGGAGAACGT TGCTGATGCC CGAAAACCAAC CTGCCTACT CCGCTACT CCGCTACT CCCGTGAGG ATGTACCC CCGTGGAGG CCCTTGGTT CCCGTTACTC CCCGTGCAGC CCCTTGGTT CCCGTTACTC CCCGTCAAGC CCCTTGGTT CCCGTTACTC CCGCTTACTC CCGCTTACTC CCCGTTACTC CCCGTTACTC CCCGTTACTC CCCTTTATTC CCAATACAAG CTTATCCGAAC CTTTTATTC CCAATACAAG CTTATCCGAAC CCTTTATTC CCAATACAAG CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CTTATCCGAAC CCACTTATTC CCAATACAAG CTTATCCGAAC CTTTATTC	AGTCAAGTTG TGCACTGGGT TGCACTGGGT AGAGGGGG GAGGCAGGGG ATTGATCCTG AGAATGGTGA ACTACAGACA ACTGCCTCAA ACTACAGACA ACTGCCGTCT CCGACTGGGC CGTACTACTT CGGCACTGGGC CGTACTACTT CGGCACTGGGC GATCAGAAAA TGTGCTCACC GGGGAGAAAA TGTGCTCACC CAGCAGTGCC GCACTGGTC CAGCAGAAAC CTGCAGTTC TCTGGGACCT TCTGGGACCT TCTGGGACCT TCTGGGACCT TCTGGCACCAA CCTGGCTTCT CACAATCAGC CAGCACTACT TCTGGGACCT TCTGCCACCAA CCTGGCTTCT CACAATCAGC CAGCACTACT CTGCCACTAAT CTGCCACTAC CAGCAGAAGC CAGCACTAC CAGCACTAC CAGCACCAA CCTGGCTCC CAGCAGACC CAGCACCAA CCTGGCTC CAGCACCAA CCTGGCGCG CAGCTGCCG CAGCACCAA CCTGGCGCG CCACACCTC CCACACCCC CCTGCCGCC CCCTGCCGC CCCTGCCGC CCCTGCCGC CCCTGCCGC CCCTGCCGC CCCTGCCGC CCCTGCCGC CCCTGCCGC CCACACCCC CCCTGCCGC CCCTGCCCC CCCTGCTGC CCCTGCCGC CCAACACCTC CCCGCCACAC CCCGTGCAG ACCCCTTAT CCCGCTCAA CCCCTTACC CCCGTGCAG CCCACACCGC CCCACACACGCT CCCGTGCAG CCCACACACGGT CCCGTCACAC CCCGTGCAG CCCACACACGCT CCCGTGCAG CCCACACACGGT CCCGTGCAA CCCGCTCACAC CCGGCACAC CCGGCACAC CCGGCACAC CCGGCACAC CCGCGCACAC CCGCGCACAC CCGGCACCAC CCGGCACAC CCGCGCACAC CCGCCCCCC CCCGCCACAC CCGCCCCCCCC	AGTCAAGTTG TCCTGCACAG TGCACTGGGT ATTGATCCTG AGAATGGTGA TACTGAACAG GCCCCGAAGT ACTGACTCC ACAGCCTTA ACTACAGACA CACTCCCCAA CACAGCCTAC CCGACTGGGC CGTACTACTT TGACTACTG GGCCACTTTT CGTACAGACA CACTGCGCC CGTACTACTT TGACTACTG GGCCACTGGC CGTACTACTT TGACTACTG GGCCACAGGGA CGTCTCCCCA GGTGGAGCG GTTCAGGCG GGTCAGAAAA TGTGCTCACC CAGTCTCCAG GGGGAGAAGG TCACCATAAC CTGCAGTCC ATACATCAC CAGGCACTC CTTACTCTC CACAATCAC CTGGCACTTA TCTGCACCAA TCTGCCACCA CCTGGCTCC CTTACTCTCT CACAATCAC CCTGGCTCC CACACCAC CCTGGCTCC CACACCAC CCTGGCTCC CACACCAC CCTGGCCC CACACCGGT CTGCCACCAA GCTGGACCC CACACCGGT CTGCCCCAC CCACACCGGT CCACACCAC CCACACCGC CCACACCGC CCACACCGC CCACACCCGC CCACACCCGC CCACACCCGC CCACACCCC CCCACACCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCGCCCC CCCCCC

Fig. 15K Nucleotide sequence of CAB1.6i gene

HICDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC (405)

L1CDR (553) AGTGCCAGCTCAGCTGTATATGCCATGCAC (582)

L2CDR (628)GATACATCCAACCTGGCTTCT(648)

L3CDR (745)CAGCAAAGAGATAGTTACCCACTCACG(771)

Fig. 15L Nucleotide sequences of CAB1.7 CDRs

		TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
1			CTTCTGGCTT	CAACATTAAA	GACTCCTATA
51	AGTCAAGTTG	GAGGCAGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
101	100101	AGAATGGTGA	TACTGAATAT	GCCCGAAGT	TCCAGGGCAA
151	77 7 01 1			CACAGCCTAC	CTGCAGCTCA
201	0000	ACTACAGACA		ATTATTGTAA	TGAGGGGCTC
251	00000	ATCTGAGGAC	CGACTACTGG	GGCCAAGGGA	CCACGGTCAC
301	CCGCTCGGG	CCATTTACAA	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
351		GGTGGAGGCG		CAATCGTGTC	TGCATCTCCA
401	GATCAGAAAA		CAGTCTCCAG	AGCTCAGCTG	TATATGCCAT
451	GGGGAGAAGG	100000	CAGGCACTTC	TCCCAAACTC	GTGATTTATG
501	GCACTGGTTC	CAGCAGAAGC	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
551	ATACATCCAA	CCTGGCTTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
601	TCTGGGACCT	CTTACTCTCT	AAAGAGATAG		ACGTTCGGTG
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	CCACACCGGT	GTCAGAAAAA
701	CTGGCACCAA	GCTGGAGCTG	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
751	CAGCTGGCGG	AGGTGGTCGC	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
801	GTCTGTTCCA	GGCATGGCGG	GATATCGCGG	CGAATAAACC	CGTTACGCCT
851	ATTACACATT	TGGCAAGGCC	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
901	CAGACCCTGT	TCGAGCTGGG	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
951	AGGTGGGGAT	GCCATTGCTC	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1001	CCAGATACTG	GCCACAGCTG	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1051	CTGGATCTCG	CCACCTACAC	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1101	TGAGGTCACG	GATAACGCCT	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1151	CGCAGTGGAA	GCCTGGCACA	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1201	CTTTTTGGTG	CGCTGGCGGT CGGGTCCTTA	AGCCGCTCAA		ACCTGGATTA
1251	CATGACGACG	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1301	ACGTGCCGAA	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1351	AAAGCGGTGC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1401	GAAAACCAAC	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG .
1451	CGGAGAACGT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1501	TCGCGCTACT	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1551	GCTCAACTGG	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1601	ATGTAGCACT	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1651	CCGGTCAAAG	GCCTTTATTC	CTGAAAAGCA		GTGATGCTCG
1701	CAGCTACGTG				ATACCATATC
1751	CGAATACAAG	CTATCCGAAC	·		
1801	CTCGAGGCGC	TACAG			

Fig. 15M Nucleotide sequence of CAB1.7 gene

	•				
1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
101	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
151	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
201	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
251	CCGCTCGGGG	CCATTTACAA	CGACTACTGG	GGCCAAGGGA	CCACGGTCAC
301	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
351	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
401	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAGCTG	TATATGCCAT
451	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATG
501	ATACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
551	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
601	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
651	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
701	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
751	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
801 851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
901 951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG		AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG		CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG		•	

Fig. 15N Nucleotide sequence of CAB1.7i gene

- H1CDR (154)GGCTTCAACATTAAAGACTCCTATATGCAC(183)
- H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
- H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)
- L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)
- L2CDR (628) AGCACATCCAACCTGGCTTCT (648)
- L3CDR (745) CAGCAAAGATCTAGTTACCCACTCACG (771)

Fig. 150 Nucleotide sequences of CAB1 CDRs

		•			
•	CAGGTGAAAC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAGGT	CAGGGACCTC
1	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
51	TGCACTGGTT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
101	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
151	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
201	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
251	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
301	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
351	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCATGTC	TGCATCTCCA
401	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
451	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	TGGATTTATA
501	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
551	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
601	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG
651	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
701	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
751 801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051		CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA		GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401-	-GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CAGCTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG	•		

Fig. 15P Nucleotide sequence of CAB1 gene

H1CDR

(26) GFNIKDSYMH (35)

H2CDR (50) WIDPENGDTEYAPKFQ (65)

H3CDR (99) GLPLGAIYNDY (109)

L1CDR (159) SASSSVSYMH (168)

L2CDR (184) DTSNLAS (190)

L3CDR (223) QQRDSYPLT (231)

Fig. 15Q Amino acid sequences of SW149.5 CDRs

- H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)
- H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
- H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC (405)
- L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)
- L2CDR (628) GATACATCCAACCTGGCTTCT (648)
- L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG(771)

Fig. 15R Nucleotide sequences of SW149.5 CDRs

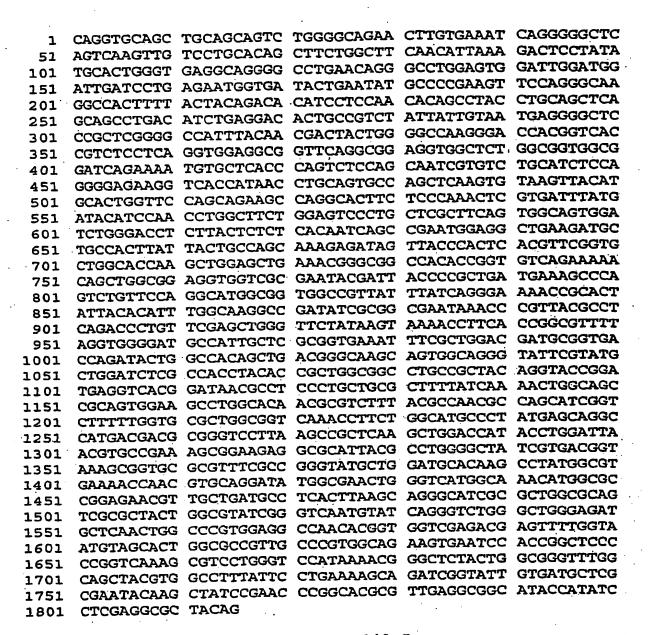


Fig. 15S Nucleotide sequence of SW149.5 gene

				•		•	
	1.	ACACCGGTGT	CAGAAAAACA	GCTGGCGGAG	GTGGTCGCGA	ATACGATTAC	
	51	CCCGCTGATG	AAAGCCCAGT	CTGTTCCAGG	CATGGCGGTG	GCCGTTATTT	•
1	01	ATCAGGGAAA	ACCGCACTAT	TACACATTTG	GCAAGGCCGA	TATCGCGGÇG	
	51	AATAAACCCG	TTACGCCTCA	GACCCTGTTC	GAGCTGGGTT	CTATAAGTAA	
2	01	AACCTTCACC	GGCGTTTTAG	GTGGGGATGC	CATTGCTCGC	GGTGAAATTT	
2	51	CGCTGGACGÀ	TGCGGTGACC	AGATACTGGC	CACAGCTGAC	GGGCAAGCAG	
3	01	TGGCAGGGTA	TTCGTATGCT	GGATCTCGCC	ACCTACACCG	CTGGCGGCCT	
.3	51	GCCGCTACAG	GTACCGGATG	AGGTCACGGA	TAACGCCTCC	CTGCTGCGCT	
4	01	TTTATCAAAA	CTGGCAGCCG	CAGTGGAAGC	CTGGCACAAC	GCGTCTTTAC	
4	51	GCCAACGCCA	GCATCGGTCT	TTTTGGTGCG	CTGGCGGTCA	AACCTTCTGG	
5	10	CATGCCCTAT	GAGCAGGCCA	TGACGACGCG	GGTCCTTAAG	CCGCTCAAGC	
.5	551	TGGACCATAC	CTGGATTAAC	GTGCCGAAAG	CGGAAGAGGC	GCATTACGCC	
6	501	TGGGGCTATC	GTGACGGTAA	AGCGGTGCGC	GTTTCGCCGG	GTATGCTGGA	
6	551	TGCACAAGCC	TATGGCGTGA	AAACCAACGT	GCAGGATATG	GCGAACTGGG	
7	.01	TCATGGCAAA	CATGGCGCCG	GAGAACGTTG	CTGATGCCTC	ACTTAAGCAG	
7	51	GGCATCGCGC	TGGCGCAGTC	GCGCTACTGG	CGTATCGGGT	CAATGTATCA	
٠ 8	301.	GGGTCTGGGC	TGGGAGATGC	TCAACTGGCC	CGTGGAGGCC		
8	151	TCGAGACGAG	TTTTGGTAAT	GTAGCACTGG	CGCCGTTGCC	CGTGGCAGAA	-
9	01	GTGAATCCAC	CGGCTCCCCC	GGTCAAAGCG	TCCTGGGTCC	ATAAAACGGG	_
9	51	CTCTACTGGC	GGGTTTGGCA		CTTTATTCCT	GAAAAGCAGA	_
10	01	TCGGTATTGT	GATGCTCGCG		ATCCGAACCC	GGCACGCGTT	
10)51	GAGGCGGCAT	ACCATATCCT	CGAGGCGCTA	CAG	** *** *** * * * * * * * * * * * * * *	

Fig. 15T Nucleotide sequence of BLA gene

1	CAGGTGAAAC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGTT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCATGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATA
- 551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
. 951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	01111110000	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA		ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC ACCTGGATTA
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT CCTATGGCGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG GGTCATGGCA	AACATGGCGC
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG		GCTGGCGCAG
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC CAGGGTCTGG	GCTGGGAGAT
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	GGTCGAGACG	AGTTTTGGTA
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	AAGTGAATCC	ACCGGCTCCC
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	GGCTCTACTG	GCGGGTTTGG
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GATCGGTATT	GTGATGCTCG
1701	CAGCTACGTG	GCCTTTATTC	CTGAAAAGCA	TTGAGGCGGC	ATACCATATC
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TIGAGGCGGC	HINCONINIC
1801	CTCGAGGCGC	TACAG		•	

Fig. 15U Nucleotide sequence of CAB1.1 gene

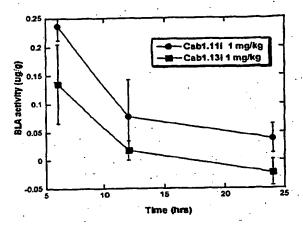


Figure 16

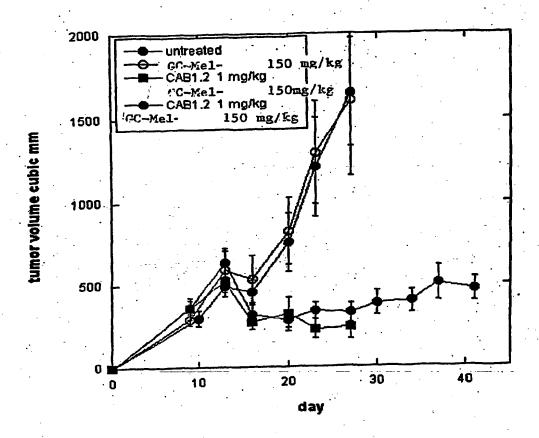
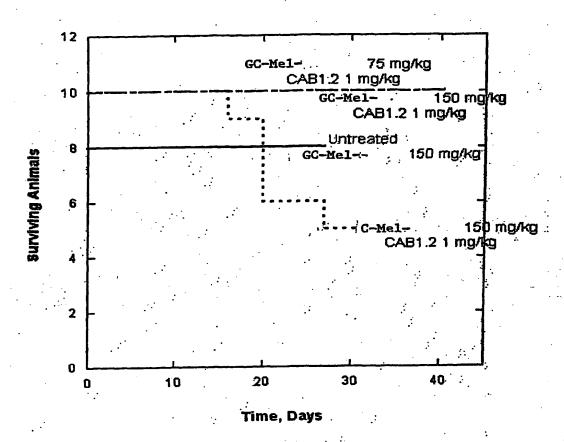


Figure 17



Jegure 18

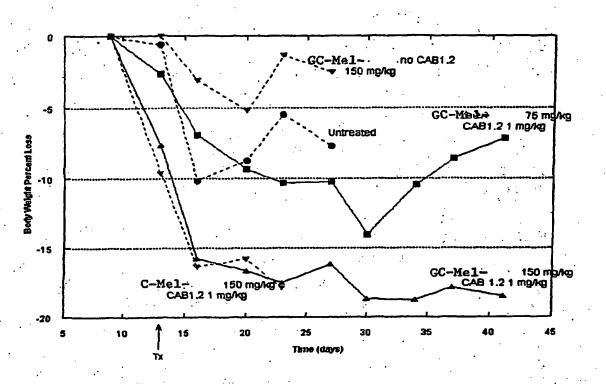
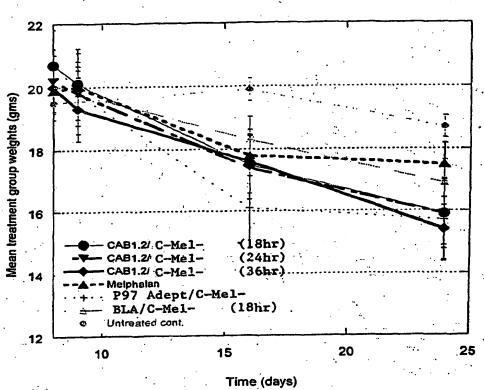


Figure 19

Animal weight effects



•

Figure 20

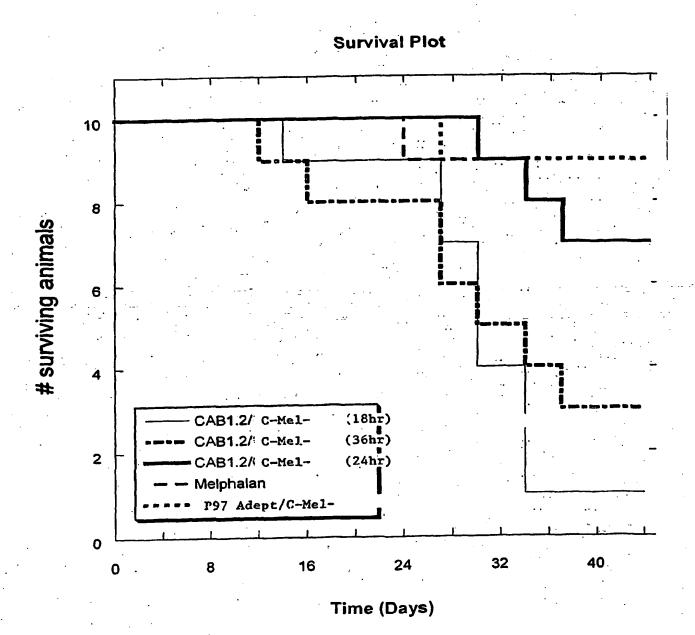
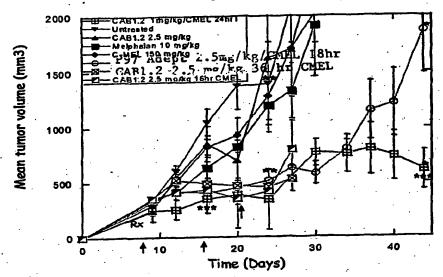


Figure 21

CAB1 Proof of Principle – Efficacy#



*p<0.05 sgn17 vs CAB1.2(24h) **p<0.05 untreated vs CAB1.2(18,24,36h)

*** GC observed in 2 animals: 1 Day 16; 1 Day 44

Legure 22

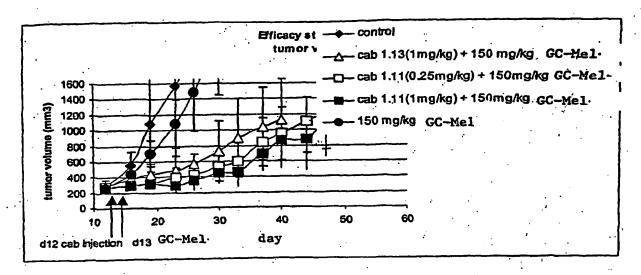


Figure 23

1	OVOLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	TOPENGOTEY	APKFOGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101	PTGPYYFDYW	GOGTTVTVSS	GGGGSGGGS	GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA			VIYSTSNLAS	GVPARFSGSG
	SCTSYSITIS	RMEAEDAATY	YCQQRSSYPL		
201	OLAEVVANTI			KPHYYTFGKA	DIAANKPVTP
251	OTLFELGSIS			DAVTRYWPQL	
301	LDLATYTAGG			NWQPQWKPGT	
351			RVLKPLKLDH		AHYAWGYRDG
401	LFGALAVKPS		VODMANWVMA		SLKQGIALAQ
451		DAQAYGVKTN		SFGNVALAPL	
501	SRYWRIGSMY		AFIPEKQIGI		PARVEAAYHI
551	PVKASWVHKT	GSTGGFGAYV	HETEROIGI	ALITICIATOTEIA	EUVANUUTIT
601	LEALQ				

Jegure 24A

•	CAGGTGCAGC	TGCAGCAGTC	TECECCAGAA	CTTGTGAAAT	CAGGGGGCTC
1	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
51		GAGGCAGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
101	TGCACTGGGT		TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
151	ATTGATCCTG	AGAATGGTGA		CACAGCCTAC	CTGCAGCTCA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA		
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC.	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751		CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC		•	•	•
1001	0.00				

Figure 24B

	OVOT ODSCAF	T.VKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
_	↑ A OTO O S G S G S G S G S G S G S G S G S G	POKEOCKATE	TTDTSSNTAY	LOLSSLTSED	TAVYYCNEGL
51	IDPENGDIEI	APREQUATE	CCCCCCCCCC	GGGGSENVIT	QSPAIVSASP
101	PLGAIYNDYW	GQGTTVTVSS	GGGGGGGG	WINCHONI DO	CADYBECCE
151	GEKVTITCSA	SSAVYAMHWF	QQKPGTSPKL	VIISISNLAS	GVPARFSGSG
201	CCMCVCT TTS	PMEAEDAATY	YCQQRDSYPL	TFGAGTKLEL	KRAATPVSEK
	OT A DURINNIM T	TOTMADOSVP	GMAVAVIYOG	KPHYYTFGKA	DIAANKPVTP
251 .	OTATANTI	TIDIMMIZOT	ATAPCETSID	DAVTRYWPOL	TGKQWQGIRM
301	QTLFELGSIS	KILIGATGGD	OMAGE TO KINE	MMODOMKDCT	TRIVANASTG
351	LDLATYTAGG	TATOA SDEAT.	DNASTTKIIA	MAGE CHILL OI	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	KATKbTKTDH	TWINVPRALE	AHYAWGYRDG
451	VAURUS PGMI.	DAOAYGVKTN	VODMANWVMA	NMAPENVADA	STYGGIATYG
	CHANNALCHA	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
501	SKIWKIGSMI	Q020		VMIANTSYPN	PARVEAAYHI
551		GSTGGFGAYV	WETERVATOR	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
601	LEALQ		*		

Figure 24C

				•*	
1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
301	CCGCTCGGGG	CCATTTACAA	CGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAGCTG	TATATGCCAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	GGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	_CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG	•		

Fegure 24D

	_		·		
1	DIVLTQSPAS	LSVSLGORAT	MSCRAGESVD	IFGVGFLHWY	
51	LIYRASNLES		SGTDFTLIID	PVEADDVATY	YCQQTNEDPY
101	TFGGGTKLEI		SGGGSGGG	SGGGSGGGG	SEVQLQQSGA
	ELVEPGASVK		KDTYMHWVKQ	RPEOGLEWIG	RIDPANGNSK
151					GYYVSDYAMA
201		ITADTSSNTA		LMAAQSVPGM	· · · · · · · · · · · · · · · · · · ·
251	YWGQGTSVTV				
301	HYYTFGKADI	1211111 1 5-	LFELGSISKT		ARGEISLDDA
351	VTRYWPQLTG	KQWQGIRMLD		LQVPDEVTDN	
401	QPQWKPGTTR	LYANASIGLF	GALAVKPSGM	PYEQAMTTRV	LKPLKLDHTW
451		YAWGYRDGKA	VRVSPGMLDA	QAYGVKTNVQ	DMANWVMANM
501		KOGIALAOSR	YWRIGSMYQG	LGWEMLNWPV	EANTVVETSF
551	GNVALAPLPV	AEVNPPAPPV	KASWVHKTGS	TGGFGAYVAF	IPEKQIGIVM
	—	RVEAAYHILE			• •
601	LANTSIPNEA	VAPWILLID			*

Jegine 25A

					•
1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTC	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC		CTGATGGCGG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACC	CTGTTCGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTCGCT	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC TCAAAACTGG
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	ACGCCAGCAT
1201	CAGCCGCAGT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	
1251	CGGTCTTTT	GGTGCGCTGG	CGGTCAAACC	TTCTGGCATG	CCATACCTGG
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	GCTATCGTGA
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG GCTGGATGCA	CAAGCCTATG
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	ACTGGGTCAT	GGCAAACATG
1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1501	GCGCCGGAGA		TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1551	GCAGTCGCGC		GAGGCCAACA		GACGAGTTTT
1601	AGATGCTCAA		GTTGCCCGTG	GCAGAAGTGA	ATCCACCGGC
1651	GGTAATGTAG	CACTGGCGCC	GGGTCCATAA	AACGGGCTCT	ACTGGCGGGT
1701	TCCCCCGGTC		ATTCCTGAAA		TATTGTGATG
1751	TTGGCGCGTA			CGCGTTGAGG	CGGCATACCA
1801		CAAGCTATCC	GAACCCGGCA	000110.100	,
1851	TATCCTCGAG	GCGCTACAG			•

Jugue 25B

Case D	ASM	Sample (D	Sample Pathology
<u> C10000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>C10000005496</u>	FF5	FR5B337147	Adenocarcinoma of lung
<u>Cl0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
		4	
<u>C17000000241</u>	AF4	ER00033A78	Adenocarcinoma of lung
<u>CI0000007518</u>	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>Ci0000008475</u>	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
<u>CI0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

Figure 26

26_B 26_C

26_G

26 JA 340

FIG. 26 -A

Case Diagnosis	Hissue of Origin/Site of Finding	∵. H	E	Anti-H
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u>	<u>20X</u>	Immunoger
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IJIB	Lung/Lung	<u>4X</u>	<u>20X</u>	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u>	20X	Anti-California Innecessaria
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung:	43	<u>20X</u>	
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated_ Stage: IIIA	Lung/Lung	<u>4x</u>	<u>20X</u>	
Adenocarcinoma of colon, metastatic Grade: Nel Reported Stage: IV	Colon/Liver	<u>4×</u>	<u>20X</u>	Immunt Fibr No No
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4</u> X	20X	

FIG. 26-3

luman Cytokeratin AE1/AE3	CAB/GCR3708 (0:2ug/ml)	CAB/GCR55
ncity: Tumor(100%, Variable to 3+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x SF00029758	Immunogencity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029756	Immunogencity: Tumor(10 Mixed inflammatory cel Necrosis(Varia Specifici 4x SF000
	Immunogencity: Tumor(15%, Variable to 3+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed Inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x SF0002975B	Immunogencity: Tumor(4 Intra-alveolar macrophat Mixed inflammatory cel Specific 4x
and have the entered of the analysis of the section detection of the entered of t	Immunogencity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF0002977F	Immunogencity: Tur Cellular stroi Chronic inflammatory or Specifici 4x SF000
	Immunogencity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Gyto). Specificity: High 4x SF00029788	Immunogencity: Tumor(6 Gellular Stroma(V: Necrosis(Varia Intra-alveolar macropha Specific 4x
	Immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x SF0002975F	Immunogencity: Tur Fibrotic stror Necrosis(Varia Specifici 4x SF000
ogencity: Tumor(98%; Variable to 3+ Mem Variable to 3+ Cyto) rolic stroma(Variable to 1+ Cyto) rmal liver parenchyma(2+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High	Immunogencity: Tumor(95%, Variable to 34 Mem; Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x 20x SF00029768 Normal liver parenchyma shows positive staining (1+)	Immunogencity: Turno Mem, Variable Fibrotic stroma(Va Normal liver pare Necrosis(Varia Specifica 4x
المنظم المنظمة المنظم المنظمة ا	Immunogencity: Tumor(85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029783	Immunogencity: Turnc Mem,Varlabli Cellular stroi Normal muscle(Va Specifici 4x

F16. 26-C

17 (0.2ug/ml)	CAB/GCR6798 (0.2ug/ml)	CAB/GCR8886 (0.196ug/
00%, Variable to 3+ Cyto) Ils(Variable to 3+ Cyto) able to 2+ EC) ity: High 20x	Immunogencity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029753	Immunogencity: Tumor(100%, Variable Mixed inflammatory cells(Variable to Specificity: High 4x SF00029754
'29757 (0%, Variable to 3+ Cyto) ges(Variable to 2+ Cyto) Ils(Variable to 2+ Cyto) Ily: High 20x 2975C	Immunogencity: Tumor(10%, Variable to 2* Cyto) Intra-alveolar macrophages(Variable to 2* Cyto) Mixed inflammatory cells(Variable to 2* Cyto) Specificity: High 4x 20x SF00029759	Immunogencity: Tumor(10%, Variable to Intra-alveolar macrophages(Variable to Mixed inflammatory cells(Variable to Specificity: High 4x 20x SF00029754
mor(100%, 2+ Cylo) ma(1+ Cyto) ells(Variable to 1+ Cyto) ity: High 20x 129780	Immunogencity: Tumor(100%, 2+ Cyto) Ceilular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF0002977D	Immunogencity: Tumor(100%, 2+ Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to Specificity: High 4x 20x SF0002977E
t5%, Variable to 3+ Cyto) ariable to 2+ Cyto) able to 2+ EC) ges(Variable to 2+ Cyto) ity: High 20x 2978C	Immunogencity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x SF00029789	Immunogencity: Tumor(75%, Variable Celtular Stroma(Variable to 2+ C) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to Specificity: High 4x SF0002978A
nor(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) ity: High 20x	Immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x SF0002975D	Immunogencity: Tumor(100%, 3+ Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x SF0002975E
x(98%, Variable to 3† e to 3+ Cyto) anable to 1+ Cyto) another to 1+ Cyto) able to 3+ EC) by: High 20x 129769	Immunogencity: Tumor(95%; Variable to 3+	Immunogencity: Tumdr(95%, Variable Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x SF00029766 Normal liver parenchymia shows positive st
or(85%, Variable to 3+ e to 3+ Cyto) ma(1+ Cyto) ariable to 2+ Cyto) ity: High 20x 129784	Immunogencity: Tumor(95%, Variable to 3+ Mem Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029781	Immunogencity: Tumor(95%, Variab Mem,Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ C Specificity: High 4x SF00029782

F16.26-D

ml)	No Antibody control (Prediluted)
to 3+ Cyto) 1+ Cyto)	Immunogencity: N/A
	Specificity: Unknown
	<u>SF00029755</u>
pro monarch communication (2015)	कर १ वर प्राप्त के जानकार प्राप्त से कर प्रकृति । जानकार से कि विकास के किया है । स्थान कर प्राप्त के जानकार से प्राप्त से कर प्रकृति । जानकार से किया है ।
to 2+ Cyto)	
o 2+ Cyto) 2+ Cyto)	
Cyto)	
1 1+ Cyto)	
. "	
to 3+ Cyto) lyto)	
∋ 2 ± Cyto)	
De Lavar	
Cyto)	
•	
ile to 3:	
yto)	
(10)	Immunogencity: N/A
	Specificity: Unknown
	<u>SF00029767</u>
taining (1+)	
ile to 3+	
yto)	
• •	
·	

FIG. 26-E

•			
erm over more person and the	1869:SED	are finally as the constraint.	e en en statuer e la colo di Università (Septembrio) de la colo di Septembrio (Septembrio) della colo di Sep
CI0000017970	HF1	FR65EE7B3D	Adenocarcinoma of colon
·		•	
C10000010013	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
		·	
C10000009651	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
C10000008690	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u> </u>			
alice occurs of the property of the	marenes en	nees seed streeth files and significant	era en magelera en malemante de la participa de la participa de la companya de la companya de la companya de l La companya de la co
C10000007678	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
C10000009736	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal
]]		

F16. 26-F

Adenocarcinoma of colen - Grade: AJCC G2: Moderately differentiated Stage: IIIC	Colon/Colon	4X	<u>20X</u>	
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X</u>	20X	Immu Fibros <u>4x</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4</u> X	<u>20X</u>	
Grade: AJCC G1: Well differentiated Stage: IIA Adenocarcinoma of pancreas, ductal	Pancreas/Pancreas	<u>4X</u>	<u>20X</u>	
Grade: AJCC G2; Moderately, differentiated Stage: III	Pancreas/Pancreas	- <u>4X</u>	<u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u>	<u>20X</u>	

FIG. 26-6

	Immunogencity: Tumor(100%, 3# Cyto) Cellular stroma(1# Cyto) Necrosis(Variable to 3# EC) Specificity: High 4x 20x SF00029787.	immunogendityi Tur Gellular siroi Necrosis(Vani Specifici 4x SF000
inogencity: Tumor(100%, 3+ Cyto) adipose tissue(Variable to 1+ Cyto) Specificity: High 20x SF0002977C	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002977A	Immunogencity: Tur Fibroadipose tissue(Specifici 4x
	Immunogencity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF6002977.1	Immunogenčity: Tur Desmoplästic stroma Specifici <u>4x</u> <i>SF000</i>
	Immunogencity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976D	Immunogencity: Tur Myxoid stroma(Va Specifici <u>4x</u> <u>SF000.</u>
	Immunogencity: Tumor(85%, Variable to 3+ Cylo) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029763	Immunogencity: Tumor(8 Celtular stroma(V): Chronic pancreatitis(Specific 4x
The state of the s	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029775	Immunogencily: Tur Chronic pancreatitis(Fibrotic stroma(Vs Specifici 4x SF000

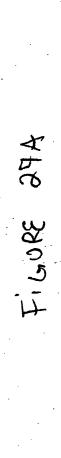
FIG. 26-H

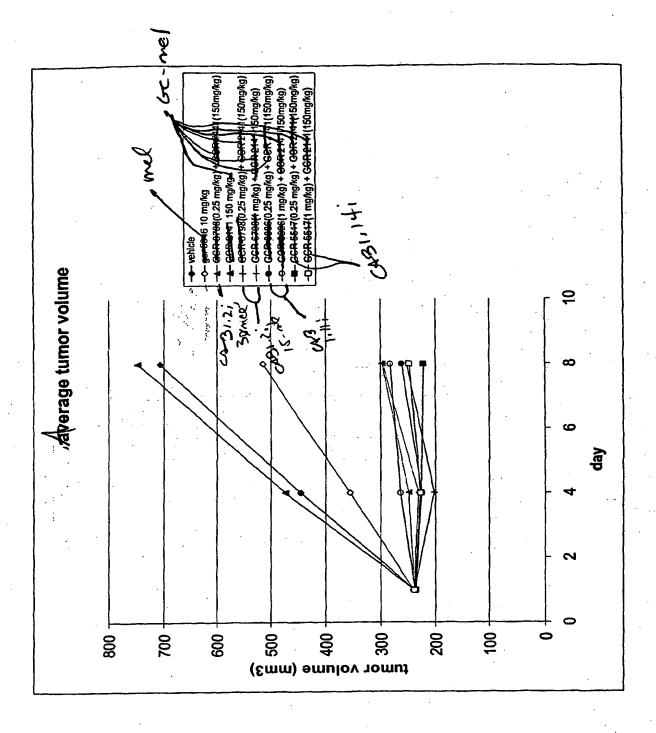
mor(100%; 3+ Cyto) ma(1+ Cyto) able to 3+ EC) lty: High 20x i <u>29788</u>	Immunogenaty: Tumor (100%; 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High 4x :20x SF00029785	Immunogencity: Turnor(100%; 3+ Cellular stroma(14: Cyto) Necrosis(Variable to:34: EC) Specificity: High 4x: 20x SF00029786
nor(100%, 3+ Cyto) Variable to 2+ Cyto) ity: High 20x 2977B	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029777	Immunogencity: Tumor(100%, 3+ Fibroadipose tissue(Variable to 2+ Specificity: High 4x 20x SF00029778
nor(100%; 3+ Cyto) (Variable to 2+ Cyto) ity: High 20 <u>K</u> (29772	Immunogencity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029770	Immunogencity: Tumor(100%; 3+ Desmoplastic stroma(Variable to 2- Specificity: High 4x 20x SF0002976F
mor(100%, 3+ Cyto) anable to 2+ Cyto) ity: High 20x 2976E	Immunogencity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x SF0002976B	Immunogencity: Tumor(100%, 3+ Myxoid stroma(Variable to 2+ C) Specificity: High 4x SF0002976C
i5%; Variable to 3+ Cyto) anable to 1+ Cyto) (Variable to 1+ Cyto) ily: High 20x 129764	Immunogencity: Tumor(85%; Variable to 3+ Cyto). Cellular stroma(Variable to 1+ Cyto). Chironic pancrealitis(Variable to 1+ Cyto). Specificity: High Ax 20x SF00029761.	Immunogencity: Tumor(85%; Variable to Cellular stroma(Variable to 1+ 0 Chronic pancreatitis(Variable to 1+ 0 Specificity; High 4x 20x SF00029762
mor(100%, 3+ Cyto) (Variable to 2+ Cyto) ariable to 2+ Cyto) ity: High 20x	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029773	Immunogencity: Tumor(100%, 3+ Chronic pancreatitis(Variable to 2+ Fibrotic stroma(Variable to 2+ C) Specificity: High 4x 20x SF00029774

F16.26-I

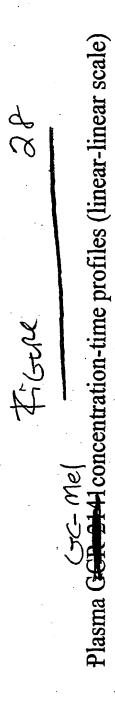
Cyto)	
Cyto) Cyto)	Immunogencity: N/A Specificity: N/A
	<u>SF00029779</u>
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F1G. 26-7

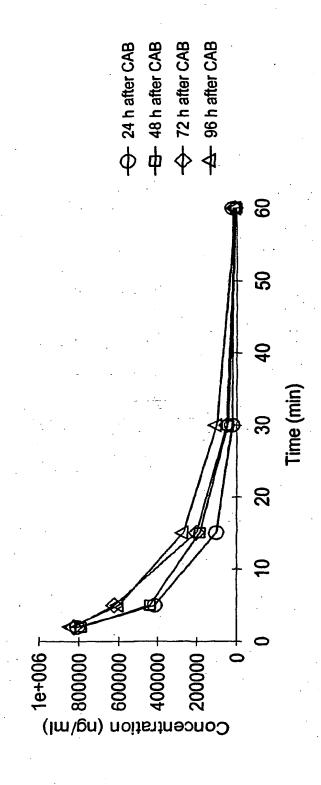


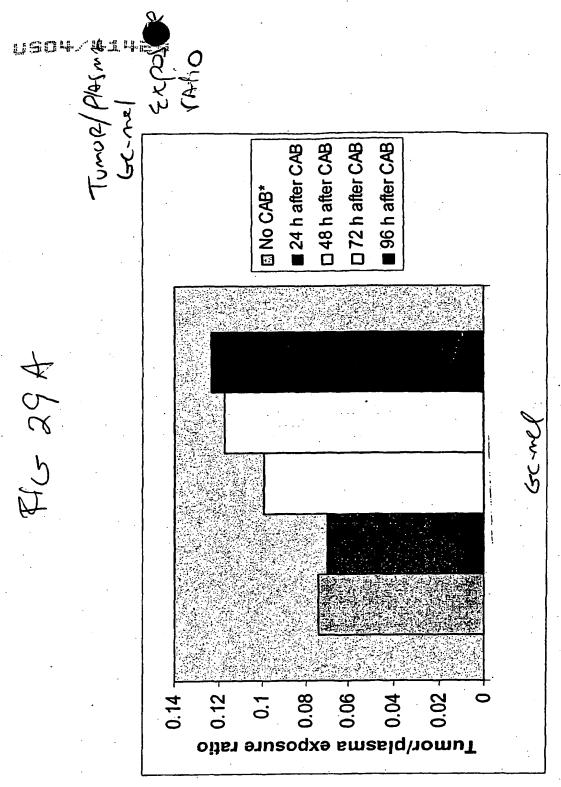


FIFTIRE 37 B

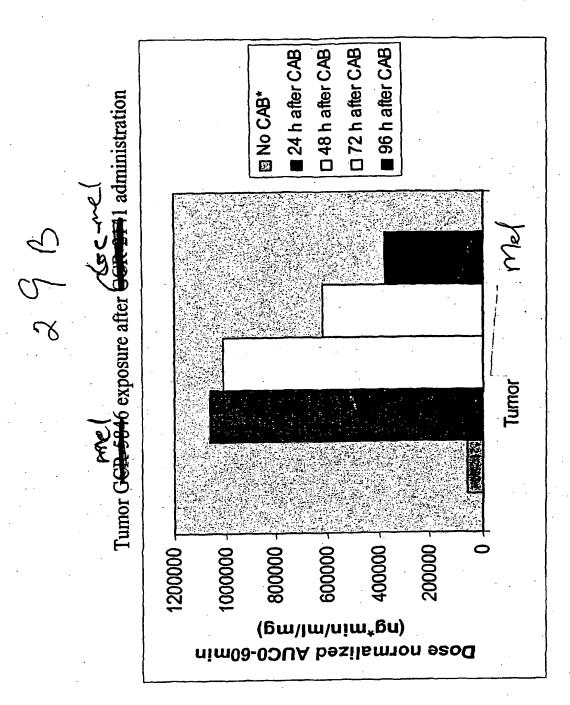


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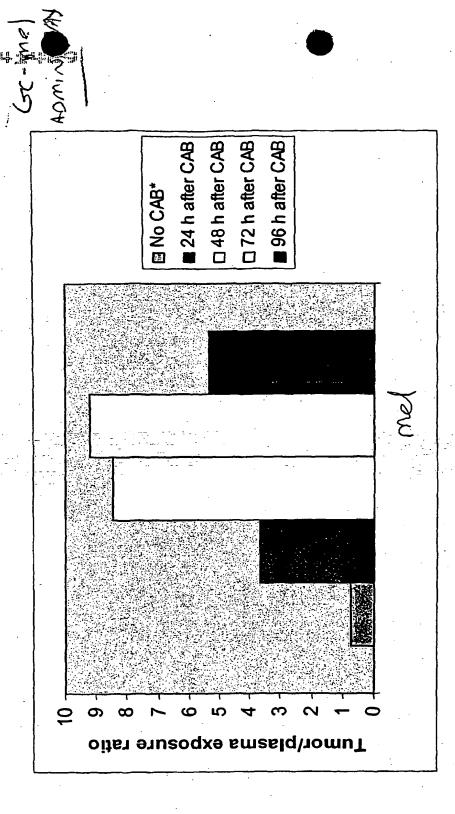




Data from study 04052, melphalan formulated in cyclodextrin



Data from study 04052, melphalan formulated in cyclodextrin



Data from study 04052, melphalan formulated in cyclodextrin

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